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X02539 Wheat gene
X00627 Wheat mRNA
U51307 Triticum ae
K03076 Wheat (T.ae
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U51306 Triticum ae
AC121410 Rattus no
AC118835 Rattus no
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Neisseria
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Polynucle
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103335 Sequence 2
X01130 Wheat gene
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AJ133611 Triticum
AJ130948 Triticum
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AC010110 Drosophil
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version:
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Maximum Match 100%
Listing first 45 summaries
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GenCore
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Neisseria meningitidis serogroup A strain 22491 complete genome;
segment 5/7.
AL162756 AL157959
AL162756.2 GI:7380091
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L (bases 1 to 329861)
Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher, Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T. Davis,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N., Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K., Ouail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M., Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G. Complete DNA sequence of a serogroup A strain of Neisserla maningitidis 22491
                                                                                                                                                                                                                                                              21 AlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle
                                                                                                                                                                                                                                                                                                                                                                      41 LysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIle
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Neisseria meningitidis 22491
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
    catarrhalis genome
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 Nucleotide sequences of moraxella catarrhalist Patent: WO 0078968-A 21 28-DEC-2000;
Incyte Genomics, Inc. (US)
Location/Qualifiers
1. 39003
/Organism="Moraxella catarrhalis"
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11568 a 8751 c 7476 g 11208 t
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Moraxella catarrhalis
Bacțeria; Proteobacteria; gamma subdivision; Moraxellaceae;
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Matches:
Conservative:
Mismatches:
Indels:
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Patent: WO 0109331-A 1 08-FEB-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
                DNA
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Sequence 21 from Patent WO0078968.
AX067446
            AX081157 405 bp
Sequence 1 from Patent WO0109331.
AX081157
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                                                   AX081157.1 GI:13170049
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Moraxella catarrhalis
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Lagace, R.E., Patterso
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PEHBYLGOLVKEKLIYYPIVSREFFEHHGRLPDLMVSGKLFEDIGLPKINPQDDRAML
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KNISFLDFEDDPSEVLTIAQCQARDWLCYIHSTALILKNGGLLEAAAEKWGGVLSDQP
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2904. .2937
//note="stem loop containing DNA uptake sequences: acgat
gccgtctgaa gcc ttcagacggc atata"
2909. .2918
//note="Core DNA uptake sequence: gccgtctgaa"
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E-value 8.4e-05"
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/protein_id="CAB84678.1"
/db_xref="GI:7380095"
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/note="Core DNA uptake sequence: gccgtctgaa"
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          complement(922. .931)
/note="Core DNA uptake sequence: gccgtctgaa"
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                                                                                                                                                                                                                                                                                                                                                    /product-"hypothetical protein NMA1441"
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/db_xref="G1:7380094"
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                                                                                                                                                                                                                                                     /note="NMA1441, len: 264 aa; unknown"
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/gene="NMA1443"
4159. .4320
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4039. .4058
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/note=">= 9
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/gene="fpr"
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/note=">= 9
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          misc_feature
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/prodein_id="CAB84675.1"
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KWRGLAYPELAFEIMRLFVTDIPEDDLRDILNRTYTEAAFGTKEITPVRTLSDGIKIQ
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TVNSINWGRIVAQVVYYFAGYFKATQSNDEQVSFCVPSGNFGNVCAGHIAKQMGLPVR
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TADGVKVAREVREERETVVCLETALAAKFDATIREAVGDVAIPRPAALEGLENLPQRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="NMAL439, possible lipoprotein, len: 123 aa;
unknown, contains a probable N-terminal signal sequence
and an appropriately positioned PS00013 Prokaryotic
membrane lipoprotein lipid attachment site"
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/codon_start=1
/transl_table=11
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Notes:
Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
Location/qualifiers
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Parkhill,J.
Direct Submission
Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
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Pyridoxal-phosphate dependent enzymes, score 231.80,
E-value 1e-65"
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/note="Core DNA uptake sequence: gccgtctgaa"

    .329861
    .7cganisma-Neisseria meningitidis 22491"
/strain-"22491"
    /db_xref-"taxon:122587"

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/gene="thrC"
/EC_number="4.2.99.2"
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/gene="NMA1439"
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/gene="NMA1439"
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/gene="thrc"
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/translation="MAAFNTQKVLSVHHWTDAYFTFTCTRDESLRFENGGFVMVGLMV
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DLNPGKHLYLLSTGTGIAPFLSITKDPEIYEQFEKIILVHGVRYKKDLAYYDRFTKEL
PEHEYLGDLVKEKLIYYPIVSREEFEHHGRLTDLMVSGKLFEDIGLFKINPQDDRAML
                                                                                                                                                                                                           Tettelin, H., Saunders, N. J., Heidelberg, J., Jeffries, A.C.,
Nelson, K.E., Eisen, T.A., Ketchum, K.A., Hood, D.W., Peden, J. F.,
Dodson, R. J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J. D.,
Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
Dougherty, B.A., Mason, T., Clecko, A., Parkesy, D.S., Blair, E.,
Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,
Plaza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Complete genome sequence of Neisserla meningitidis serogroup B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:L36319 PID:540280 percent identity: 86.05; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
     of 206
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  Neisseria meningitidis serogroup B strain MC58 section 97
                                                                                                                                                                        Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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complement(1675. .2469)
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20175755
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/db_xref="taxon:122586"
/note="serogroup: B"
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                                                                                                                        Neisseria meningitidis MC58.
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112. 318
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                      the complete genome.
AE002455 AE002098
AE002455.1 GI:7226282
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KEYWORDS
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                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                     APPase, len: 823 aa; similar to many e.g. SW:COPA_ENTHR APPase, len: 823 aa; similar to many e.g. SW:COPA_ENTHR (EMBI:Lil292), copA, Enterococcus hirse Copper/potassium-transporting APPase A (EC 3.6.1.36) (727 aa), fasta scores; E(): 0, 34.0% identity in 744 aa overlap. Similar to NMA1539, fasta scores; E(): 0, 34.4% identity in 735 aa overlap. Contains hydrophobic, probable membrane-spanning regions. Contains two Pfam matches to entry PF00122 E1-E2_AFPase, E1-E2_AFPases and PS00154
                                                                                                                                                                                                                /translation~"MIYKKNCPNKKCYAENKMKRWVFIENGCSATVIHRTGIWKKIIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCT 25-MAY-2000
                      unknown, lies within a region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative P-type cation-transporting ATPase"
/protein_1d="CAB84680.1"
/db_xref="GI:7380097"
/db_xref="SPTREMBL:Q9JU88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 ATCGTCAAAATGGCGGTAGAAAGCCAATGCCGTGCGGAATTGAACAAACGCAGCGAATGG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 CGTTTGACCGCGCTGGCGATGAGTGCCGAAAAACAGGCGGAATGGGAAAACAAGATTTGC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AlaSerThrProGluSer----AsnProLysAsnSerSerAlaAsnLeuThrThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 ATGAATAAAACCTTGTCTATT-----TTGCCGGTGGCAATCTTACTCGGCGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LyslleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 GlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla
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29
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                                                                                                                /product="hypothetical protein NMA1443"
/protein_id="CAB84679.1"
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Mismatches:
Indels:
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                 /note="NMA1443, len: 53 aa; u
of unusually low GC content"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                /db_xref="GI:7380096"
/db_xref="SPTREMBL:Q9JU89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-048-196-2 (1-134) x NMA5Z2491 (1-329861)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                 /gene="NMA1444"
complement(4509. .6980)
/gene="NMA1444"
                                                                                                                                                                                                                                                                  complement(4509. .6980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11489 bp
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118.00 .
47.118
23.148
17.468
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 TGC 544
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LOCUS
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/product="transposase, IS30 family"
/protein_id="AAF41448.1"
/db_xref="GI:7226290"
/translation="MSYTQLTQGERYHIQYLSRHCTVTEIAKQLNRHKSTISREIRRH
RYQGQOYSARKAQRQSQTIKQRRRQPYKLDSQLIQHIDTLIRRKLSPEQVCAXLCKHH
QITLHHSTIYRYLRQDKSNGSTLWQHLRICSKPYRKRYGSTWTRGKVPNRYGIENRPA
IVDOKSRIGDWAADTIVGKOGXSALLTLYLDRYRYRYTICKLDSLKAEDTARAAVRALK
AHKDRYHTTMDNGARFYCHRITKALKAETYFCRPYHSWEKGLNENTNGLIRQYFPK
QTDPRNISDREIRRVQDELNHRPKTLGYETPSVLFLNLFQPLIH"
complement (8805. 10715)
                                                                                                                                                                                                                                                                           TPLFRRTGKGMVLTRAGEILLPEAESLLQYKHKLEHFAKTLAGDYSEETSLGIIHPID
SAKIVALTDNIGQTARKTRIAIQYGMSGEILSRIQHKTLHGGFILGMAAQRGIRSVFL
QNLTYALICPOSOY PHLTRSLPQSLQECVWIEMSGVSGSRKHLHQFWRSNRLSPKKQI
LCDYQRIIDLVAGGIGVAWVPGNKAEAAAKEGAGVAIIESCRHSMPLNFIYAEEYED
NPHVSLLLECIEKVWGVQAVQPPVVSDN"
COMPLEMENT (7718. .8683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATRIVELDRGILRSYPGSFSKYSEKRAQELAVEAEHNRLFDKFHAQEEAWIRKGIEA
RRTRNEGRYRRLEELRRQRAERRNVGGVNFKLDSGEKSGKITALEEHASFAYGGKVI
MDFFSAILQRGDKIGLIGPNGIGKTFEKLILGELQPTGRIRIGSKQEVAYFDGFRS
ALNENDTVFYTLGGOMYVEVGGKKHYWAYLEDFLEHARAQSPVSELSGGERNRLL
LAKLFTRPANILVLDEPTNDLDIDTQELLEDLLRDYQGTVFLVSHDRMFLDNVITQSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MNILSVENASFAIGHVALLDKTSFQLDSGEKVGLIGRNGAGKSS
FLKILAGLQKLDDGQIIVQNNLKIVYVPQESFFDKDATVFDTVAEGLGEIRDLLRRYH
HVSHELENGSSEALLKELNELQLEIEAKDGWKLDAAVKQTLGELGLPENEKIGNLSGG
                            PID:148255
                                                                                                                                                                                                                                                    /translation="MDAVQLKSFVAVAHEGNLTQAAKRLFLSQPAVSAQIKALEEYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKKRVALAQAWVQKPDVLLLDEPTNHLDIDAIIWLENLLKAFEGSLVVITHDRRFLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to GB:L42023 PID:1007269 PID:1221430 PID:1205538 SP:Q57242 percent identity: 69.46; identified by sequence similarity; putative" /codon_start=1 /transl_table=11
                            SP:P23841 GB:X63976 PID:14825948.44; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GB:L27157 PID:451858 percent identity: 62.86; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="ABC transporter, ATP-binding protein,"
/protein_id="AAF41449.1"
./db_xref="G1:7226291"
                                                                                                                                                                   /product="transcriptional regulator, putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111489
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Mismatches:
                            /note="similar to GB:M13687
PID:41595 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
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                                                                                                                                                                                          /protein_id="AAF41447.1"
/db_xref="GI:7226289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="NMB1051."
complement(8805..10715)
/gene="NMB1051"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="NMB1050"
complement(7718. .8683)
/gene="NMB1050"
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                                                                  /codon_start=1
                                                                                                                                         /transl_table=11
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116.00
46.28%
23.97%
17.16%
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Best Local Similarity:
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TVNSINWGRLVAQVVYYFAGYFRATGSNDETVSFCVPSGNFGNVCAGHIAKQMGLPIR
KLIVATNENDVLDEFFKTGAYRPRNSAHTYVTSSPSMDISKASNFERFVFDLMDRDPA
ELNTLWAEVAAGKGEPLRFALDKVGGKYGFTSGKSTHADRLATIKOYYEQDOELIDPH
TADGVKVAREVREGEBWVVCLETALAAKFDATIREAVGDAAIPRPAALEGLENLPQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"hypothetical protein"
/protein_id="AAF41445.1"
/d_xref="G1:7226281"
/translation-"WHXTLGILPVAILLGGCAAGGGNTFGSLDGGTGMGGSTVKMAVG
SQCRAELDKRSEWRLTALAMSAEKQAEWENKICACVAQEAPERMTGNDVMQMLAPSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSGFFLPGANLPGTHGPLIPMIPIVVSAGGHPLAFGISIAVLGLLMALFRGGSIMAKL
TSNGVCGGLLLYLGFIGTTGQVKKLFSWAGGFNMPYIAPTVIIVTIVMYALLEHWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPFAVLAVAMWSPDFLGHQVFQKISYPEKTDKVLMNIDDTMTSCSVRQAVGSILGGAN
FTSSWGTYIVPASIAKRPIPGGAVLTAVLCIIAGLWGYPMDLAIWQPVLSVALVVGVY
                                                                                                                                                                                                                                                                                                  NARWRYALLGWYARYIKLGVLKPVPSLGGEPAIATESKRLYELRSAGIAVPELLAVRK
NALMEGNLEGOTPLDAQIROBREAGKSDAWLAGLEAIARVHKRQFLSQAFARNAMSDG
KNISFLDFEDDPSEVLTIAQCQARDWLCYIHSTALILKNGGLLEAAAEKWGGVLSDQP
AEIOKLIAATVKPLIETRREBPRWGRDALRLAASISLISLADMPP"
complement(2515. .3924)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to SP:P23669 GB:X56037 PID:580784
PID:580991 percent identity: 71.31; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation = "MKYISTRGETAHKPFSEVLLMGLAPDGGLMLPEHYPQIGRETLD
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ALSNGPTLAFKDMAMQFLGNAFEYVLNKEGKKLNILGATSGDTGSAAEYALRGKKGVN
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                                                                                                                                                                                                                                                                                 /translation="MTLPMQETRFSILLDELAAKQEAAIAPHLLADGTKVWIRKAGRH
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/note="hypothetical protein; identified by Glimmer2;
putative"
                                                                                   'note="hypothetical protein; identified by Glimmer2;
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                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="AAF41443.1"
/db_xref="G1:7226285"
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/transl_table=1
/product="hypothetical protein"
/protein_id="AAR41446.1"
/db_xref="G1:7226288"
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/db_xref="GI:7225286"
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/gene="NMB1047"
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/gene="NMB1047"
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complement(4620. .6089)
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/transl_table=11
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/gene="NMB1049"
6345. .7259
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'trans1_table=11
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                                                   'gene="NMB1045"
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/gene="NMB1045"
complement(1675
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:CMB9-99M9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 164197 ATGAATAAAAACCTTGTCTATT-----TTGCCGGTGGCAATCTTACTCGGCGGCTGC 164147
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CGTTTGACCGCGCTGGCGATGAGTGCCGAAAAACAGGCGGAGTGGGAAAACAAGATTGC 4138
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79 GlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla
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                                                 LyslleAlaAlaMetLysLeuSerSerGluSerLysAlaLyslleSerGluThrAlaCys
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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/db_xref="taxon:487"
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Conservative:
Mismatches:
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86755 c 95584 g 86290 t
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Query Match:
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AX044031/c
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Published Only in Darghase (1999)

E 2 (bases 1 to 68466);

Hattori,M., Ishli,K.; Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujlyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakaki,Y.
Fujlyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakaki,Y.
Direct Submission

L Direct Submission

L Submitted (08-NoV-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKBN), Genomic Sciences Center (GSC):
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-855,
Japan (E-mail:hattori@gsc.riken.go.jp/, Tel:81-42-778-9923,
Rax:81-42-778-9924)

On May 31, 2000 this sequence version replaced gi:6997560.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP000686 68466 bp DNA linear HTG 30-MAY-2000
Homo sapiens chromosome 11 clone CMB9-99M9 map 11q25, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                               DD 163909 CTGGCTCCGTCCACGCGCAATCAGGCACTTGCCGCCCTGACGCCCAAAACGGTTTCCGCC 163850
                                                                                                                                                                                                             163966 GCTTGCGTCGCCCAAGAAGCACCCGAACGATGACCGGCAACGATGTG---ATGCAGATG 163910
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact. hattori@gsc.riken.go.jp/
Conter project Information
Center project name: Humbraftii
Center clone name: CMB9-99M9
Center project name: Paranersham: 100% of reads
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 66248 bases at least 030
Consensus quality: 66348 bases at least 020
Consensus quality: 66946 bases at least 020
Insert size: 67366; sum-of-contigs
Quality coverage: 8.74x in 020 bases; sum-of-contigs
                                                                                                                                                                     79 GlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla
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Hattori, M., Ishli, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens 68,466 genomic DNA.of 11q25
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58471. .61089
//note="assembly_fragment"
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34596. .41662
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41763. .48030
/note="assembly_fragment"
41763 48030 contig of 6268 bp in length
48131 53188 contig of 5058 bp in length
53289 58370 contig of 5082 bp in length
61890 6374 contig of 2619 bp in length
6186 65573 contig of 1729 bp in length
6731 68466 contig of 1729 bp in length
6731 68466 contig of 1136 bp in length
6731 68466 contig of 1136 bp in length
6731 68466 contig of 1136 bp in length
8 NOTE: This is a 'working draft' sequence. It currently
8 consists of 12 contigs. The true order of the pieces
8 is not known and their order in this sequence record is
8 runs of N. but the exact sizes of the gapes are unknown.
8 This record will be updated with the finished sequence
8 soon as it is available and the accession number will
8 be preserved.
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a 14973 c 14428 g 18666 t

    14889
    /note="assembly_fragment"
    14990. .27066

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/clone="CMB9-99M9"
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ORIGIN
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AC079123 187087 bp DNA linear HTG 19-AUG-2000 Homo sapiens chromosome 11 clone RP11-507F16, WORKING DRAFT SEQUENCE, 14 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 187087)
                                                                                                                                                                                                                         25971 TTAAGGCTGATGATCATCACAGCCACAGTAATGCAACTGTCTTCAGCAGCACTAGAACTG 26030
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                                            Conservative:
Mismatches:
Length:
Matches:
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                                                                                         Indels:
                                                                                                               Gaps:
                                                                                                                                                       US-10-048-196-2 (1-134) x AP000686 (1-68466)
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Waterston; R.H.
                  103.50
36.88%
27.66%
15.31%
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                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                            Quality coverage: 4.81 in Q20 bases; agarose-fp Quality coverage: 4.59 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s; gap of unknown length
): contig of 9442 bp in length
): gap of unknown length
: contig of 11501 bp in length
; gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t: gap of unknown length
c: contig of 6268 bp in length
c: gap of unknown length
contig of 9166 bp in length
gap of unknown length
                Sequencing vector: plasmid; 0% of reads Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminators Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: bases at least 040 Consensus quality: bases at least 030 Consensus quality: bases at least 020 Insert size: 193000; agarose-fp Insert size: 185787; sum-of-contigs
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gap of unknown length
contig of 21416 bp in length
gap of unknown length
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of 13808 bp in length
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gap of unknown length
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152608: gap of unknown length
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/note="assembly_name:Contig13
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/note="assembly_name:Contig17"
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note="assembly_name:Contig15"
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/chromosome="11"
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Sequencing vector: M13; 100%
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gap of
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AP003327 188041 bp DNA linear PRI 08-MAR-2002
Homo sapiens genomic DNA, chromosome 11g, clone:RP11-507F16,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                               Conservative:
Mismatches:
Indels:
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152609. .187087
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a 41318 c 39330 g 51421 t ]
                 61440. .77318 //note="assembly_name:Contig20" 77419. .98834
'note-"assembly_name:Contig19"
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Matches:
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Homo sapiens
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36.88%
27.66%
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Best Local Similarity:
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TITLE Homo sapiens genomic DNA JOHRNAL, Published Only in Darahase (2001)	Eukaryota; Me Mammalia: Pui
REFERENCE 2 (bases 1 to 188041) AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.	REFERENCE 1 GRESS 1 I AUTHORS DOE Joint Ger TITLE Direct Submis
TITLE Direct Submission JOURNAL Submitted (23-FEB-2001) Masshira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@qsc.riken.go.jp, WIE.ihttp://hqp.qsc.riken.qo.jp,)	JOURNAL Unpublished REFERENCE 2 (bases 1 i AUTHORS DOE Joint Ger TITLE Direct Submis
Tel:81-45-503-9111, Fax:81-45-503-9170) COMMENT On Mar 7, 2002 this sequence version replaced gi:13122444. FEATURES Location/Qualifiers Source 1188041 /organism="Homo sapiens"	
/db_xref="taxon:9606" /chromosome="11" /map="11q" /clone="RP11-507F16" DASE COUNT 57134 a 41996 c 39470 g 49441 t	Drive, Walnu COMMENT On Oct 23, 28 Draft Sequen www.jgi.doe.g Finishing Co
Alignment Scores: 95.5 Length: 188041 Pred. No.: 103.50 Matches: 39 Score: 103.50 Matches: 39 Percent Similarity: 36.88% Conservative: 13 Best Local Similarity: 27.66% Mismatches: 52 Query Match: 15.31% Indels: 37 Description: 15.31% Ganes: 52	Cuality: Phre Cuality: Phre Estimated Too FEATURES Loca Source 1. Or. Adb.
-10-048-196-2 (1-134) x AP003327 (1-188041)	BASE COUNT 73389 a 5 ORIGIN
Qy 2 MetLysIleLeuTyrValThralaThrLeuMetThralaPheThrLeuaka 18 ::::::::::::::::::::::::::::::::::::	Alignment Scores: Pred. No.: Score:
Qy 19	Percent Similarity: Best Local Similarity: Query Match: DB:
Oy 27 AsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaVal 44	US-10-048-196-2 (1-134) : Qy 2 MetLyslleLeuTy
Qy 45 LysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaalaMetLys 64	Db 27637 TTAAGGCTGATGAT Qy 19
Qy 65 LeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys 84	Db 27697 ACACATGGCATGGG' Qy 27 ASnProLysAsnSe.
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Qy 105 ThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThrVal 124	Db 27802 AAAAGAGAGAGTGC Qy 65 LeuSerSerGluSe
Oy 125 Asn 125 	Db 27835 TTACAGAGCCCTCTC Qy 85 AlaproGlualaVa
9 1 290	27
. X 2	Oy 105 ThrGluValAlaGlu
KEYWORDS HTG. SOURCE Homo sapiens. ORGANISM Homo sapiens	Qy 125 Asn 125 Db 27997 AAT 27999

inssion 15-SEP-1999) Production Sequencing Facility, DOE Joint itute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA to 238472) 123-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell ult Creek, CA 94598, USA 2001 this sequence version replaced gi:7711412. Since Produced by DOE Joint Genome Institute Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; iutheria; Primates; Catarrhini; Hominidae; Homo. to 238472; enome Institute and Stanford Human Genome Center. GTCAGAGTGGAATATGCAGGAAGTCCTGCCTTGACATTCCTCATCTG 27756 ------ACGACCATACTGTTTCGGGGGAAACATGCCAGC 27801 CTACCTTTATGGAAGGT----CCC 27834 alSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArg 104 InLysIleValArgHisSerLeuLysProCysMetLeuGluThrVal 124 -----SerCysAlaSerThrProGluSer 26 erLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys 84 InThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLys 64 erSerAlaAsnLeuThrThrSerLeuIle-----LysHisAlaVal 44 enome Institute and Stanford Human Genome Center. .gov ompleted at Stanford Human Genome Center 238472 339 113 52 37 5 anford.edu rrap Quality >=40 99.7% of Sequence: Otal Number of Errors is 0.5. ocation/Qualifiers Length:
Matches:
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Indels: lone="CTB-125B20" 52011 c 48279 g 64793 rganism="Homo sapiens" b_xref="taxon:9606" hromosome="5" x AC010290 (1-238472) enome Institute. to 238472) 128 103.50 36.88% 27.66% 15.31% ission ission

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

AB058719 LOCUS

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL

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Maruyama,N., Ichise,K., Katsube,T., Kishimoto,T., Kawase,S.,
Matsumura,Y., Takeuchi,Y., Sawada,T. and Utsumi,S.
Identification of major wheat allergens by means of the Escherichia
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QQQAQNVVHXIILHQQXQQQQPSSQVSFQQPLQQFGSFRPSQQNPQDGSVQ
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Triticum aestivum gene for alpha-gliadin mature peptide, complete
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Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                   2083 TCTACTGTCTCCACGGCCACTAGTTTACCTTCTGTTGCCAGCACTCCCGCAGCTCCAAAC 2142
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                                           9 AlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSer---Asn 27
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alpha-gliadin mature peptide; alpha-gliadin.
Triticum aestivum (cultivar:hard red spring ICW) DNA.
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/product-"alpha-gliadin mature peptide"
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Eur. J. Biochem. 255 (3), 739-745 (1998)
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Sobara,O., Nagase,T. and Kikuno,R.

Sobara,O., Nagase,T. and Kikuno,R.

Direct Submission

L. Submitted (27-MAR-2001) Osamu Ohara, Kazusa DNA Rsearch Institute,

Department of Human Gene Research; 1532-3, Yana,

Soldis, Japan (E-mail:cdnainfo@kazusa.or.jp,

URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,

Fax:81-438-52-3914)

Soldis: Fax:81-438-52-3914

Corganism="Homo sapiens"

Ab_xref="taxon:966"

//Lisue_type="brain"

//Lisue_type="brain"
                                                                                                                                                                                                                                           Nagase,T., Nakayama,M., Nakajima,D., Kikuno,R. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 8 (2), 85-95 (2001)
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RLPEIKLPVNGCSDLEDSFTILQSKDLKQEPLDDPTCIDTSETSLSNQNKLFSDINLN
DQEWQELIDELANTVPEDDIQDLFNEDFEEKKEPEFSQPATETPLSQESASVKSDPSH
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SQSVVDANTGTVRTLNPAAMGRQMMPSLPGQQGTSQARPMVMSGLSQGVPGMPAFSQH
PAQQQIPSGSFAPSSQSQAYERNAPQDVSYNYSGDGAGGSFPGLPDGADLVDSIIKGG
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QQHPSKPQQDAEAASAEQRNHTLIMLQETVKRKLEGARSPLNGDQQNGACDGNFSPTS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              linear Printial cds.
                AB058719 5164 bp mRNA lines
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA j (bases 1 to 249846) MCPherson, J.D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Aug 8, 2002 this sequence version replaced gi:21492356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 249846)
MCPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                              360 GGATGTTGTATTGCAGCAACACAACATAGCGCATGGAAGATCACAAGTTTTGCAACAAAG 419
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/note="N-terminal primer region for PCR" 765. 780 //note="C-terminal primer region for PCR" 246 c 119 g 155 t
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31
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                Chemistry: Dye-primer ET; 08 of reads
Chemistry: Dye-primer ET; 08 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 240797 bases at least 040
Consensus quality: 242108 bases at least 030
Consensus quality: 242698 bases at least 020
Insert size: 248095; sum-of-contigs
Quality coverage: 10.08 in Q20 bases; sum-of-contigs
of 11239 bp in length
unknown length
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Sequencing vector: plasmid; 100%
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/clone="RP23-42113"
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IleAsnProAsnAlaArgThrGluValAlaGlnLysIleVi: GTCAGAAGCAGTTCAGCTCATACACACACTCCTGCAAACTGC LysProCysWetLeuGluThrValAsnAlaPhelleValProThrI	BASE COUNT 166 a 215 c 133 g 114 t 4 others
misc_feature //note="assembly_name:Contig33" misc_feature //note="assembly_name:Contig84" misc_feature //note="assembly_name:Contig86" misc_feature //note="assembly_name:Contig86" misc_feature //note="assembly_name:Contig86" misc_feature //note="assembly_name:Contig80" misc_feature //note="assembly_name:Contig80" misc_feature //note="assembly_name:Contig90" misc_feature //note="a	Alignment Scores: Pred. No.: Scores: 1.34e+03

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FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Oct 25, 2001 this sequence version replaced gi:16303526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R. H.
Direct Submission
Submitted (25-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                  Louis,
                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (18-OCT-2001) Genome Sequencing Center. Washington
University School of Medicine, 4444 Forest Park Parkway, St.
Mo 63108, USA
4 (bases 1 to 174410)
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                                                                                                                                                                                                                                    (bases 1 to 174410)
Tomlinson,C., Haglund,K. and Spalding,L.
The sequence of Homo sapiens BAC clone RP11-21M10
Unpublished (2001)
(bases 1 to 174410)
                                                                                                                                                            Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                              Chordata; Primates;
                                                                                                                                       Sulston, J.E. and Waterston, R.
  AC097464.3 GI:16418223
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                                                                                                                     (bases 1 to 174410)
                                                           Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                           Homo sapiens.
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/rpt_family="Ar_rich"
10323. 10487
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10737. 10809
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/rpt_family="(TG)n"
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12228. 12367 1695. .9214 'note="similar to EST 8019. .8067 /rpt_family="AT_rich" 8695. .9214 /rpt_family="Alu" 12826. .13022 /rpt_family="MIR" 13099. .13266 /rpt_family="CR1" 14001. .14312 /rpt_family="MIR" |3373. .13664 rpt_family="Alu" 3695. .13766 family="Alu" .9187 9161. repeat_region misc_feature MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
MCPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc NOTICE: This sequence may not represent the entire insert of this folore. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. The RECI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanaes, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: pBACe3.6

SOURCE INFORMATION:

```
The clone sequenced to the left is RP11-342I1; the clone sequenced to the right is RP11-328NB. Actual start of this clone is at base position 1 of RP11-21M10; actual end is at base position 174410 of RP11-21M10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
4337. .4853
/note="similar to EST AW173298 (NID:g6439246) xj85g01.xl"
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                                                                                                          Data from AC044906 and AC040995 was used to finish this clone, AC019343. Polymorphisms have been identified between AC044906, AC040995 and AC019343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠,
                                                                                                                                                                                    The sequence of AC019343 has been incorporated into AC097464
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                                                                                                                                                                                                                                                                                                                                                                                                             EST BG571049 (NID:g13578702)"
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بنه
NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                        /organism="Homo saplens"
/db_xref="taxon:9606"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5234, .5886
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1192. .1244
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                                                                                                                                                                                                                           source
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Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu ------ Summary Statistics

Center project name: H_NH0021M10 Drafting Center: WIBR

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AL845171 226325 bp DNA linear HTG 09-AUG-2002
Mus musculus chromosome 4 clone RP23-38N8, *** SEQUENCING IN
PROCRESS ***, 13 unordered pieces.
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 226325)
                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:22035729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator; 100% of reads
Consensus quality: 218645 bases at least Q40
Consensus quality: 221861 bases at least Q30
Consensus quality: 221861 bases at least Q30
Insert size: 225174; 235723 bases at least Q20
Insert size: 225774; 1.7% error; agarose-fp
Quality coverage: 5.27x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10851 10950; gap of 100 bp 10951 40599 40699; gap of 100 bp 40599 40699; gap of 100 bp 40699 88025; contig of 47327 bp in length 88126 103225; contig of 15100 bp in length 10326 103325; gap of 100 bp 100 bp 103326 117128; contig of 13803 bp in length 103326 117128; contig of 13803 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7228: gap of 100 bp 120412: contig of 3184 bp in length 10512: gap of 100 bp 145346: contig of 24834 bp in length
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contig of 20476 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10850: contig of 10850 bp in length
                                             Db 99209 GCAGTGACAGTGGCCGGTTCAGCGTCAGGGCCTGTGGCTGT 99169
                      80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coverage: 5.29x in Q20 bases; agarose-fp
                    67 erGluSerLysAlaLysIleSerGluThrAlaCysGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: UK-MRC
Web site: http://mrcseq.har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: mouseq@har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200407: gap of
220883: cont
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HTG; HTGS_PHASE1.
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200408
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                                                                                                 RESULT 15
AL845171/C
                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSer---Asn 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 ProLysAsnSerSerAlaAsn-LeuThrThrSerLeuIleLysHisAlaValLysGlnTh 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7949. .28439
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Matches:
Conservative:
Mismatches:
Indels:
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30318. 30660

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8964. .19002
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715. .19863
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16389, 16/11
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                                                                                                                                                                                                                                                                                                                                      pt_family="MIR"
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92.50
54.678
38.678
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Query Match:
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38 SerLeuIle-----LysHisAlaValLysGlnThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1210 others
220884 220983: gap of 100 bp
220984 226325: contig of 5342 bp in length.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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92.00
38.10%
25.00%
13.61%
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                                FEATURES
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DD 114299 CTCTCGAAGCTTTTGTGGTTCACAGCAACCAGGACCTGCTTGATCTTTTATGAATAGC 114240

Db 114239 ATATTCTCTAGAGTCAGTGTACCTGCTATTTGAGCAATGAATCTTCTAGCCTTACAATT 114180

21 AlaSerThrProGluSerAsnPro-----LysAsnSerSerAlaAsnLeuThrThr 37

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Direct Submission

Louding (02-FBB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
on Feb 5, 2001 this sequence version replaced gi:1265262.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw.; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP, Information on the WORMPEP database can be found at PRI 02-FEB-2001 http://www.sanger.ac.uk/HGP/Chri3
FIL-223E19 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: PAAAC3.6
IMPORTANT: This sequence is not the entire insert of clone RPI1-223E19 It may be shorter because we sequence overlapping 113952 114060 114059 TTCTCTTATCCATTTGTCTATTGGGATTTTCATGTTTTCAATGGTATGATGATGATTTTTA 114000 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 62043) http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 102 103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122 62 AL161893 62043 bp DNA linear PRI 02-1 Human DNA sequence from clone RP11-223E19 on chromosome 13, 63 MetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAla Db 113999 CAGTTAGTGCTTGCAATCTCAAAAGCCAAAATTTCTACCAATGACTGT-------83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn .--LysileAlaAla 48 -----CysGlnThrGlnLeu: ------ThrGlyHis Mapping Group. Further information can be found at Db 113861 TTGGTAAATGAGGTGATTTTCCCC 113838 123 ThrValAsnAlaPheIleValPro 130 complete sequence. AL161893 AL161893.24 GI:12666231 Homo sapiens Bates, K. DEFINITION ORGANISM AUTHORS TITLE JOURNAL 26 RESULT 16 ACCESSION REFERENCE VERSION KEYWORDS SOURCE

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note="LlME1 repeat: matches 5763. .6112 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                               551. .3709
note="L1MD3 repeat: matches 7566. .7729 of consensus"
once, except for a 100 base overlap.
end of clone RP11-550P23 is at 61944 in this
true right end of clone RP11-374F3 is at 100 in
                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clromesome="13"
/clone="RPI1-223E19"
/clone="MER66A repeat: matches 97. .486 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                               1712, .3862
fnote="Alusq/x repeat: matches 1, .151 of consensus" 863, .3902
                                                                                                                                                                                                                                                                 .359 of consensus"
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Anote="WER69 repeat: matches 335. .395 of consensus"
                                                                                                                                                                                                                                                                                72. .1149
note="AluSx repeat: matches 1. .285 of consensus"
150. .1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7912. 9798
7001e="AluSx repeat: matches 3. 296 of consensus" 8924. 10230
7001e="AluSx repeat: matches 1. 306 of consensus" 7001e="AluSx repeat: matches 1. 311 of consensus" 7001e="AluSx repeat: matches 1. 311 of consensus" 7001e="Milk repeat: matches 8. 186 of consensus" 70112. 11315
                                                                                                                                                                                                                                                                                                                              note="MLT1B repeat: matches 1. .326 of consensus"
672. .1974
note="AluSx repeat: matches 5. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="20 copies 2 mer aa 77% conserved"
305. .4207
octe="AluSx repeat: matches 2. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                              192. .3482
note="AluSx repeat: matches 1. .291 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MER20 repeat: matches 1. .218 of consensus"
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note="MIR repeat: matches 35. .237 of consensus"
2474. .12785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151. .5733
octe="HAL1 repeat: matches 1. .588 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 47. .120 of consensus"
                                                                                                                                                                                                                                                                 matches 326.
                                                                                                                                                                                                                                                38. .871
note-"MLT1B repeat:
                                                                Location/Qualifiers
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/note="MIR r
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Lregion Mote-WireS0 repeat: matches 507. .654 of consensus."

Lregion Mote-WireS0 repeat: matches 224. .2511 of consensus."

Lregion Mote-WireS0 repeat: matches 10. .299 of consensus."

Lregion Mote-LiMBH repeat: matches 11. .295 of consensus."

Lregion Mote-LiMBH repeat: matches 11. .295 of consensus."

Lregion Mote-LiMBH repeat: matches 11. .295 of consensus."

Lregion Mote-Miss repeat: matches 11. .295 of consensus."

Lregion Mote-TiME repeat: matches 11. .295 of consensus."

Lregion Mote-Miss repeat: matches 11. .295 of consensus."

Lregion Mote-Miss repeat: matches 11. .295 of consensus.

Lregion Mote-Miss repeat: matches 12. .295 of consensus.

Lregion Mote-Miss repeat: matches 13. .295 of consensus.

Lregion Mote-Miss repeat: matches 13. .295 of consensus.

Lregion Mote-Miss repeat: matches 12. .295 of consensus.

Lregion Mote-Miss repeat: matches 13. .295 of consensus.

Lregion Mote-Miss repeat: matches 12. .295 of consensus.

Lregion Mote-Miss repeat: matches 12. .295 of consensus.

Lregion Mote-Miss repeat: matches 2. .69 of consensus.

Lregion Mote-Miss repeat: matches 2. .69 of consensus.

Lregion Mote-Miss repeat: matches 2. .69 of consensus.

Lregion Mote-Miss repeat: matches 11. .209 of consensus.

Lregion Mote-Miss repeat: matches 12. .295 of consensus.

Lregion Mote-Miss repeat: matches 13. .295 of consensus.

Lregion Mote-Miss repeat: matches 13. .257 of consensus.

Lregion Mote-Miss repeat: matches 13. .257 of consensus.

Lregion Mote-Miss repeat: matches 13. .290 of consensus.

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Wheat (T.aestivum) alpha-/beta-gliadin class A-II mRNA, complete cds, clone pA212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma-type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wheat (T.aestivum, cv. Cheyenne) seed, cDNA to mRNA, clone pA212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 ArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThr 123
10000 ACAGGAAAGAGCGCTTACTTAACTCTGCGCTTGGCACTTGACAAATGTTTATTGGCTACC 20059
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 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLys---LeuSerSerGluSer
                                                                       /note="AluSq repeat: matches 3. .294 of consensus' 38193. .38272
/note="MIR repeat: matches 67. .146 of consensus" 40216. .40395
/note="MIR repeat: matches 23. .223 of consensus" 40868. .41833
/note="CPG island"
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1 (bases: Troiticum.)

0kita,T.W., Cheesbrough,V. and Reeves,C.D.

Evolution and heterogeneity of the alpha-/beta-type and gar
                                     of consensus
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 .501
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/note="Charlielb repeat: matches 35. 36403. 36709
                                                                                                                                                                                                                                                Length:
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Conservative:
Mismatches:
Indels:
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J. Biol. Chem. 260 (13), 8203-8213 (1985)
85234522
                                 /note="AluSx repeat: matches 1. 36721. .37004
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/translation-*MKTFPILALLAIVATTATTAVRVPVPQLQLQNPSQQQPQEQVPL
VQEQQFQGQQQPFPPQQPPFPSQQPYLQLQPFPQPQLEYPQPQPFRPQQPYPQ
PQPOYSQPQOPD ISQQQQQQQQQQQQQQILQQILQQQLIPROVVLQOHNIAHGSSQV
LQESTYQLVQQLCQCQLWQIPEQSRCQAIHWVHAITLHQQHHHHQQQQQQQQQQQ
QVSFQQPQQYPSGQGFFQPSQQNPQAQGSFQPQQLPQFEEIRNLALQTLPAMCNVXI
Sequence divergence between the classes is due to single base substitutions and to duplications or deletions within or near direct repeats. There are more than a hundred copies of the gene encoding alpha 'Deta-gladin per haploid genome. Amplification or rearrangement of DNA does not occur during development, since
                                                                                                hybridization patterns are the same, whether DNA isolated from leaves or seeds is used.

Potential polyadenylation signals are present at 1017-1022 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 AlaValLysGlnThrCysGlnThrGlnLevThrGlyHisGlnTyrTrpLysIle----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----CAGGGATGTTGTATTGCAACAACAACATAGCGCATGGAAGCTCACAAGT
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41
                                                                                                                                                                                                                                                                                            64. .939
/note="pre-alpha-/beta-gliadin A-II"
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/product="alpha-/beta-gliadin A-II"
5 a 229 t 181 g 229 t bustream of PstI site; chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                             1. .1102
/organism="Triticum aestivum"
/db_xref="taxon:4565"
<1. .1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA34276.1"
/db_xref="GI:170712"
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                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 CysMetLeuGluThrValAsnAla 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPYCTIAPFGIFGTN"
                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.63
89.50
37.84%
24.32%
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Best Local Similarity:
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123 bp u
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DB:
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No..
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                                                                                                                                                                                                                                                          mRNA
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DEFINITION ACCESSION VERSION

LOCUS

RESULT 18 LMFL163/c

g

ORGANISM

KEYWORDS SOURCE

AUTHORS

REFERENCE

98146435

MEDLINE PUBMED

JOURNAL TITLE

TITLE JOURNAL

AUTHORS

REFERENCE

Notes

COMMENT

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GAYASPADLLPARKAAASULDMFHRESQORTNGGYACVRGTPVCEPSHQVIPASC
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GAIGVDYREEGGIISSVAGDASNFGRASAAEHAQSRATLGSLFGPPHGAVAWGVE
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STARMLQDTMSAVHLLDITVWDASELSTQVVCAALMKHPPPDVALVKFIEFLKKG
STARMLQDTMSAVHLLDITVWDASELSTQVVCAALMKHPPPDVALVKFIEFLKKG
NIDAYDLMLDYGIABEESTLBILCKOSRMEYAKLHFTVLKNNANMSATQAHSSPSP
PPRSPLASGGAGVAPVHTSAAASTSTAASRRRDERSYFAQRIEELAERRFKRASLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYHVTFRADLSGTEKWFSYFAVIVGTKTGPLDLGIGLFAASLALSDKTVNPKVATKLT
AKRDSSEHVIEAIAELEKCGWDYHRILFCDALMLEPQERASAEKNESPAGANGAGSRD
HHHGRGANGSHAAGAVASSAAAAGEEHLGKESIYTSAGQGPSSYNNSHLLSARPSLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADLVSRCSAPHFRTSAFLNVTADKDPKQEVTLSYHLMTDDAFGYGIIGAKAVSRRDGH
AALDELAALFKKMFVEPPSTLNPKLADVFVRPARDLLMKYSSGAAAGSAENKVKKVKL
AVDEVKNMALDNVERVIQRGQRIDDIVQATDDLQFQAEGFQRSSRDLRNQMWSSMKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALKVLHRAEVEGTSLEGDTYIMSALLRHYCRSTTPRHYLVLPFSESLAYRPGPVSDGV
RASAIFWEGGORKGHPAAMORPDLGPDANEELLEGEGKSAWNEELEGLEGAPTRSRGG
EPEABKGRRFRPRORDPYFADSSEEGTYILEVLKSYGSYPDNSVLAALSGYPDHSCYGDVPH
MEIVASAADAFFEGCMASHGTMSPVDCRFLHALGYYYIDNRWRDRAHLLVRRVLEMFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="L163.06"
/note="L163.06, len = 256 aa, possibly synaptobrevin-like protein; carboxy terminus exhibits reasonable similarity to several, e.g. CAB71004 synaptobrevin-like protein (240 aa, Arabidopsis thaliana, EMBL: AL132957, CAB71004); Fasta scores: E():3.3e-09, 43.2% identity in 81 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MASNVNEESHALYGAVVVRLVDRVMLCKTPSAPMDGFT1PSTAW
            because we arrange for
    overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.
Cosmid Li63 is overlapped at the 5' end by L6294 (AL354533).
THIS ANNOFATION IS PRELIMINARY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="possible synaptobrevin-like protein"
/protein_id="CAB95269.1"
/db_xref="GI:8744981"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L163.04, len > 834 aa, unknown"
                                                                                                                                                                                                                                              /organism="Leishmania major"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="L163.06"
complement(10203. .10976)
                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:5664"
/chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(<1. .2505)
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complement(1. .2505)
/gene="L163.04"
                                                                                                                                                                                                                                                                                       /strain="Friedlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=L163.06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label-L163.04
                                                                                                                                                                                                             .27081
                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          see http://www.sanger.ac.uk/Projects/L_major/
CDS are numbered using the following system eg L163.01. L163
(COSmid name). 01 (first CDS)
To make the cosmid library Leishmania major Friedlin DNA was
partially digested with Sau3AI prior to cloning into BamHI site of
the cosmid shuttle vector CLHVG (Ryan et al. 1993 Gene
131:45-150). The sequence of the packaged vector was determined by
Peter Myler and Ken Stuart at Seattle Biomedical Research
Institute, and is available as accession number US931.
The more significant matches with motifs in the PROSITE database
are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
Usually the highest scoring match (cound by fasta -o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 15A, (E-mail: barrell@sanger.ac.uk) and GATC GmbH, Fritz-Arnold-Str 23, p-78467 Konstanz, Germany see http://www.ebi.ac.uk/parasites/leish.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Hexamer program which was written by Richard Durbin as an integral part of the ACEDB-based analysis tools for the C.elegans Genome Sequencing Project. The program calculates the log-likelihood score for a given DNA segment based on the frequency of 6-mers, normalised for the base-pair composition of the genome. The program was trained using a fasta file of confirmed Leismania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Where possible we choose an initiation codon (atg) which is preceded by a stretch of pyrimidines or part of a Kozak sequence. If this cannot be identified we choose the most upstream initiation
                                                                                                                                                                INV 23-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Details of leishmania sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major coding sequences (CDS), i.e. from ATG start codon to the stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the FramePlot program of Bibb et al.,
Gene 30:157-166(1984) as implemented
at http://www.nin.go.jp/
jun/cgi-bin/frameplot.pl. (2)
codon preference based on the codon usage table for Leishmania at
http://www.kazusa.or.jp/codon/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-JUN-2000) European Leishmania major Friedlin genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION: We may not have predicted the correct initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane domains were predicted as implemented at the TMHMM Server: http://www.cbs.dtu.dk/Services/TMHMM-1.0/
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ivens, A.C., Lewis, S.M., Bagherzadeh, A., Zhang, L., Chan, H.M. and
Smith, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 27081)
Hilbert, H., Wedler, H., Wedler, E., Duesterhoeft, A., Ivens, A.C.,
Ouall, M., Rajandream, M.A. and Barrell, B.G.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                        chromosome assembly protein; synaptobrevin-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suring...
A physical map of the Leishmania major Friedlin genome
Genome Res. 8 (2), 135-145 (1998)
                                                                                                                                                            LMFL163 27081 bp DNA linear
Leishmania major Friedlin chromosome 21 cosmid L163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene prediction is done using:
762 GGGCTTCTTCCAACCATCTCAGCA 785
                                                                                                                                                                                                                                                                               GI:8744978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leishmania.
1 (bases 1 to 27081)
                                                                                                                                                                                                                                                                                                                                                             Leishmania major.
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25 GluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaVal 44
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AC127124/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
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TSANAPASASSTGARASASSPRDLESNAGGLSSKILNGSGSGGPSTET TSJILL
TSANAPASASSTGARASASSPRDLESNAGGLSSKILNGSGSGGPSTDETKVUL
TSANAPASSASSTGARVENTGNYNOVGSTLEGLØREHKDLATRERSLRSKLAKVEG
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HEREDALRSLORKLEDDETLOFSLACSNVSRLCTGAKGEDVGSTDAAAATEA
OEATEKAFAELQTKYHKRQQAAWEAAHDHAAAAAAYVVNYRRYVMSNVPHSNYDAV
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TRAARASSSDAGAVTPAAAFTYTSAHPFVSAALLVRNAKCSVAYETARASGPGGGATVV
TETQVAYAKLTTDGYBAYTAEAQDSRSALSNREAALDKLOQOGRLQFNNTLAKGEKAEL
VQAQLVAKMQHQGGFALEKDVHVLVQEAATAKLVAAGDVALVEMLQOLGVLAAAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSGGELPPPNIHHTDTIRNAVSGTSVMATVRQVFGGAVQATTLOTLHIGADGESFGF
RURSYFLINGTKLALVALUPHDTPLHMGTPLLINSSNSHATYAQLRFYTGQRFYTGGNFEGD
SIRGDGCYTENPABLESLGKLEGTDBTTGASIIVDNNPFISALEAGDLLITYVYTMO
SFLINQTNCWRLMAEAVWCMDGDDVGLDPRYMGSGAPGLAAWTESRDDPTVYPKSUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mrlprotflrropnlsgcrarpptsyssmslfvlavilavcvag
SLftvvhakdcitrgpnsmiawkyedgsfqcdncigahavgvssgtvrrrwteydkdr
Nilnsfveehregkklvlhdesrgmsillrsdlsgirtegeqtfrqlxsgafisvvdc
                                                                                                                                                                                                                                                                                                  GKOWGSAGGTGASSATKTGGSASNTSGSSSONPSAGVPPGFPPGFDLQKLQTMQQLFN
SQPKEKQEQMMKQAMEMQKMMSKIPGFGKLAQSSTKVLEQLMKMQQQAPPPSSLSTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MRCVRVLLHGKLSYPVGTGRLALGTALLPLLPSNDIFYDPAKLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / RLDQDGYLYFKNTVPRDVVNAALDDLATQMRECGLTLDEDRARQAELNGFAMGVPYP
                                                                                                                 /note="L163.07, len = 678 aa, unknown; uncertain
translation start point may use M113 (double methionine)"
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complement(19248. .20324)
/gene="L163.08"
/note="L163.08, len = 357 aa, unknown"
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38
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/note="1163.09, len = 160 aa, unknown"
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complement(23013. .>27080)
                   complement(16129, .18168)
/gene="L163.07"
complement(16129, .18168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(19248. .20324)
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Best. Local Similarity:
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LeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrPro 24

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R MARTALDA, Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alabrooks S.L., Amaratunge, H.C., Are, J.R., Ayele, M. Banks, T., Barboroks, S.L., Amaratunge, H.C., Blankenburg, K., Bonnin, D., Burbart, J., Bimage, K., Blankenburg, K., Bonnin, D., Bunde, S., Briver, M., Brown, M., Bryan, M. Bryant, N.P., Bunde, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Carcor, C., Coyle, M.D., Dathornes, S.R., David, R., Davila, M.L., Davis, C., Davyla, M.D., Dathornes, S.R., David, R., Davila, M.L., Davis, C., Davyla, M.D., Daderich, D. A., Douthwaite, R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Davis, C., Davarda, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaguards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaguards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaguards, C., Hamilton, K., Harris, K., Harris, K., Harris, M., Harlak, P., Hawes, A., Hennandez, J., Harris, C., Harris, K., Harth, M., Havlak, P., Hawes, A., Hennandez, O., Hodgson, A., Holues, M., Holloway, C., ijackson, L.E., Jacobson, B., Jaja, Y., Johnson, R., Johlay, C., Korvah, J., Kovar, C., Luja, K., Luis, R., Martinez, D., Martsinez, E., Karlsson, E., Kalls, Y., Mares, S., Hennandez, O., Lucier, R., Lun, R., Lun, R., Martinez, M., Marbar, P., Martina, R., Martinez, D., Lu, X., Lucier, R., Lun, R., Lun, R., Martinez, M., Martinez, P., Martina, R., Martinez, M., Martinez, P., Martina, R., Martinez, M., Martinez, P., Martina, R., Martina, R., Martinez, P., Martina, R., Martina, R., Martina, P., Martina, R., Martina, R., Martina, R., Martina, P., Martina, R., Martina, R., Martina, P., Martina, R., M
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
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***, 59 unordered
AC127124
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Rattus norvegicus
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NOTE: This is a working draft's sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                        Norley, K.C. Direct Submission Submitted (23-JUL-2002) Human Genome Sequencing Center, Department Submitted (23-JUL-2002) Human Genetics, Baylor College of Medicine, One Pavlor Plaza, Houston, TX 77030, USA
                                                                                                                                              Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 184024)
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,Y., Wu,Y., Wu,Y., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                         Day of Plaza, Houston, TX 77030, USA
On Jul 18, 2002 this sequence version replaced g1:21744043.

Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: GLRJ
Center clone name: CH330-173B13
Center clone name: CH330-173B13
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 139590 bases at least Q40
Consensus quality: 145742 bases at least Q30
Consensus quality: 150380 bases at least Q20
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be preserved.
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PC C12N1;
PC C12N3;
PC C12N3;
G06F15/40
CC Stranc
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7 JP 201501833-A/28
1 JP 201501833-A/28
1 30-OCT-1997 JP 1998520718
7 31-OCT-1996 US 60/029960
CT-RIES A KUNSCH,GIL H CHOI,PATRICK J DILLON,CRAIG A ROSEN,
STEVEN C BARASH,
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1 (bases 1 to 5857)

Kunsch,C.A., Choi,G.H., Dillon,P.J., Rosen,C.A., Bara,S.C.,
Fannon,M. and Dougherty,B.A.

Polynucleotide of Streptococcus pneumoniae and sequence
Patent: JP 2001501833-A 28 13-FEB-2001;
                                                                                                                                                                                                                                          57267 ATTTTGGCCATATTTGGATCCACAAGGTGGGGTATCCAATACTCAGCCTCTTTTTCT
                                                                                                                                                                                                                                                                                                                                             AlaAsnLeuThrThrSerLeuIle-----LysHisAlaValLysGlnThrCysGln---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Folynucleotide of Streptococcus pneumoniae and sequence. BD003708 and Sequence. BD003708. G1:18631669 bp. 201501833-A/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 uLysProCysMetLeuGluThrValAsnAlaPheIleValProThrThr 133
                      contig of 4873 bp in length
gap of unknown length
contig of 6051 bp in length
gap of unknown length
contig of 4017 bp in length
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Mismatches:
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OS Unidentified
PN 42 2001501833-A/28
PD 13-FEB-2001
PF 30-OCT-1996 US 60/OP
PI CHARLES A KUNSCH, GIL H
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Tettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R.J., Durkin, A.S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, J.D., Umayam, L.A., White, O., Salzberg, S.L., Lewis, M.R., Radune, D., Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A., Feldblyum, T.V., Angiuoli, S., Dickinson, T., Whitekey, E.K., Holt, I.E., Loftus, B.J., Yang, F., Smith, H.O., Fraser, C.M.
                                                                            C12N5/10,C12P21/02,C12Q1/68,G06F17/30,C12N15/00,C12N5/00, PC
MICHAEL FANNON, BRIAN A DOUGHERTY
C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4776 ATGGACAGTAAGGTCAACCGTTTATAAGAACTCAAGCAGCAAAGGCTATACTTGAACAA 4717
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5016 AATGAAAATGATAACCTTACGTCCAAGCAAATTAAAATTCATAGATGCCATGGTTACGAG 4957
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Streptococcus pneumoniae TIGR4
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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228
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    .5857
    /organism='Unidentified'

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Mismatches:
Indels:
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Streptococcus pneumoniae TIGR4
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1173 c 814 g 2
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AE007414 AE005672
AE007414.1 GI:14972604
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5516. .5968
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                                                                                                                     E 2 (bases 1 to 11849)

S Tettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D.,

Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R.J.,

Durkin, A.S., Gwinn, M., Colonay, J.F., Nelson, W.C., Peterson, J.D.,

Umayam, L.A., White, O., Lewis, M.R., Radune, D., Holtzapple, E.,

Khouti, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A.,

Feldblum, T. W., Angluoli, S., Gesuwan, P., Hickey, E.K., Holt, I.E.,

Loftus, B.J., Ujwal, M.L., Yang, F., Smith, H.O., Venter, J.C.,

Duugherty, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M.

Lougherty and P. Rockville, MD 20850, USA

Location/Qualifiers
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                             pneumoniae
Science 293 (5529), 498-506 (2001)
21357209
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Rattus,

Rat
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                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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On Jul 9, 2002 this sequence version replaced g1:20467446.
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                                                        AC111203.5 GI:21716965
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                                                                              HTG; HTGS_PHASE1
                                                                                                             Norway rat.
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                                                                                                                                                                                                                     Rattus.
                                                                                                                                   . ORGANISM
                         ACCESSION
VERSION
KEYWORDS
SOURCE
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Rattus norvegicus clone CH230-7H1, *** SEQUENCING IN PROGRESS ***,
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8502 ATGGACAGTAAGGTCAACCGTTTATAAGAACTCAAGCAGCAAAGGCTATACTTGAACAA 8561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||| ::: ||||||||||:::
8262 AATGAAAATGATAACCTTACGTCCAAGCAAATTAAAATTCATAGATGCCATGCTTACCGAG 8321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8442 ACAACTCAAATGCTTTATTTAGCATCATCTAACGCTGTTTCTGTACTCAATGATATTATG 8501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 ThrThralaalalleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHis 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 TrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAla---LysIleSerGluThr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGlu-----Leu 94
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/gene="SP1139"
/gene="SP1139"
/gene="SP1139"
/note="identified by Glimmer2; putative"
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/gene="SP1138"
/note="identified by Glimmer2; putative"
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/product="hypothetical protein"
/protein.id="AAK75248.1"
/db_xref="GI:1497615"
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/gene="SP1137"
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                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 17895 bases at least Q40
Consensus quality: 182795 bases at least Q30
Consensus quality: 188082 bases at least Q20
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/protein_id="aa25593.1"
/db_xref="G1:21755"
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Wheat gene for storage protein gliadin (A-gliadin subgroup).
X01130
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Anderson,O.D., Litts,J.C., Gautier,M.F. and Greene,F.C. Nucleic acid sequence and chromosome assignment of a wheat storage protein gene Nucleic Acids Res. 12 (21), 8129-8144 (1984) 85502803
                                                                       .laArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
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TCCTTCCAACAGGGCTCTGCAACAATA-----TCCATTAGGCCAGGGCTCTTCCG 1490
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/note="imp. inverted repeat D'"
1640...1650
/note="imp. direct repeat E"
1651...1661
/note="imp. direct repeat E"
1710...1715
/note="pot. polyadenylation signal"
/note="pot. polyadenylation signal"
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/note="storage protein (aa 1-286)"
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gliadin; inverted repeat; storage protein.
Triticum aestivum.
Triticum aestivum
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1. .2347
Aorganism="Triticum aestivum"
/db_xref="taxon:4565"
53. .61
/note="inverted repeat A"
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700. 18724 inverted repeat D"
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/note="imp. inverted repeat B"
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/note="inverted repeat A'"
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/note="inverted repeat C'"
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/note="inverted repeat C"
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/note="pot. TATA-box"
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9
               TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
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AL844497
HTG: HTGS_PHASE2; HTGS_ACTIVEFIN.
Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza; 1 (barsoideae; Oryzeae; Oryza; 1 (barsoideae; Oryzeae; Oryza; Choisne, N., Orjada, G., Cattolloo, L., Demange, N., Wincker, P., Segurens, B., Pelletler, E., Scarpelli, C., Salanoubat, M.,
                                                                                                                                                                                                                                                                                                                                                                                            1089 GTATTCGCAACCAACCAATTTCACAGCAGCAGCAGCAGCAGCAGCAACA 1148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1311 ATGGCAGATCCCTGAGCAGTCGCAGGCCATCCTCAAAGTTGTTCATGCTAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 Ile-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer----
                                                                                                                                                                                                                                                                                                                                                                        7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAla----
                                                                                                                                                                                                                                         2347
36
18
52
38
6
                                          /note="polyA site in cDNA clones"
2002. .2006
/note="inverted repeat F"
/note="inverted repeat F"
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2017. .2021
                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
.793. .1828
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                                                                                                             /unce-"inverted repeat G"
/note-"inverted repeat G"
2022. .2026
./note-"inverted repeat G'"
./note-"inverted repeat G'"
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88.00
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Best Local Similarity:
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                             misc_feature
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No. ..
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Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.
                                                                                                                          Direct Submission
Submitted (O2-AUG-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Aug 11, 2002 this sequence version replaced gi:21953218.
IMPORANT: This sequence is unfinished and does not necessarly
represent the correct sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pleces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 SerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 31145: contig of 31145 bp in length 31146 31245; gap of 100 bp 77566 77665; contig of 46320 bp in length 77566 7865; gap of 100 bp 77666 85328: contig of 7663 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31145 bp contig from 1 to 31145
46320 bp contig from 31246 to 77565
7663 bp contig from 77666 to 85328
14726 bp contig from 85429 to 100154
57108 bp contig from 100255 to 157362.

* NOTE: This is a 'working draft' sequence. It currently
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Conservative:
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         sequencing
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45547 a 32463 c 32507 g 46443 t
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/sub_species="japonica"
/db_xref="taxon:4530"
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Oryza sativa chromosome 12
Unpublished
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123 ThrValAsnAla 126
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TSP130948
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/protein_id="CAB76963.1"
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IMOIPEDSOCOALHWVHAILIHOQOKOOOPSSOVSFOOPIGOSSFRPSOON
POAGGSVOPOOLPOFEEIRNLALQTLPAMCNVYIPPYCTIAPFGIFGTNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z (bases I to 810)
Arentz-Hansen, E. H.
Direct Submission
Submitted (05-MAR-1999) Arentz-Hansen E. H., Institute of
Immunology, University of Oslo, Rikshospitalet, N-0027 Oslo, NORWAY
Location/Qualifiers
                                                                                                                                                                                                                    06-MAR-2000
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poodeae; Triticae; Triticum. (bases 1 to 810)
                                                                               41352 AATACCCTGTGCACGACCAACAAAAAGGCTCTCCA-----ACTCCTCTTGCACCATAAAC 41299
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                                                             rThralaalaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSe 115
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alpha-gliadin storage protein,
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 uThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuTh
                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of a panel of recombinant gliadins for the characterisation of {\tt T} cell reactivity in coellac disease
                                                                                                                                         115 rLeuLysProCysMetLeuGluThrValAsnAlaPheIleVal 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      function="wheat storage protein"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
/strain="Mjoelner"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="endosperm"
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257 c 125 g 15
                                                                                                                                                                                                                  TAE133611 810 bp Triticum aestivum gene encoding
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                                                                                                                                                                                                                                                                                         alpha-gliadin; storage protein.
Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="alpha-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                              AJ133611.1 GI:7209262
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87.00
36.81%
25.00%
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                                                                                                                                                                                                                                                  clone alpha-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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Query Match:
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REFERENCE
AUTHORS
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75
                                                           95
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                                                                                                                                                                                   RESULT 26
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/product="alpha-gliadin"
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/db_xref="SPTREMBL:092P09"
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VQQQQFLGQQOPEPPQQPYPQPPPSQQPYPQQQQQQQQQQQQQLIPCQQLIPCQDLIPCQVLQQPYPQ
PQPQYSQPQDPISQQQQQQQQQQQQQQQQQQQLIPCQQLIPCQDVLQQHIAH
GRSQVLQQSTYQLLQQSCQCQQHQWQDPQQQQQQQQQLIPCQRQQQQQSSQQVS
PQQPLQQSTPYQLLQQCCQHWQIPEQSQCQAIHKVVHAIIIHQQQKQQQQQSSQVS
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Triticum aestivum subsp. spelta.
Triticum aestivum subsp. spelta
Triticum aestivum subsp. spelta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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Kasarda, D.D. and D'Ovidio, R.
Deduced amino acid sequence of an alpha-gliadin gene from Spelt
wheat (Spelta) includes sequences active in celiac disease
Cereal Chem. 76, 548-551 (1999)
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Universita della Tuscia, Via San Camillo de Lellis I-1100 ITALY
Location/Qualifiers
                                                                                                                                                              422
                                                                                                                                                                                                                                                                                   482
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                                                  321 ACAACAACAACAACAACAACAAATCCTTCAACAAATTTTGCAACAACAACTGATTCCATG 380
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39
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                                                                                                                                                                                                                                                           83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S88 CTCCTTCCAACAGCCTCTGCAACAATA----TCCATTAGGCCAGGGCTCCTTCCG
-----SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu
                                                                                                           IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys
                                                                                                                                                                                                                                                                                                                                            -----GluThrAlaCysGlyCysValAla
                                                                                                                                                                                                                                                                                                                                                                                               183 ATGGCAGATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAATGTTGTTCATGCTAT---
                                                                                                                                                                                                                       60 Ile-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer----
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/variety="arduin1"
/db_xref="taxon:58933"
/chromosome="6"
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218. .>1081
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/clone_lib="pTS63"
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Seguent Seguen	SE COUNT 569 a 436 c 263 g 404 t	Qy 22SETHAPPOGLUSEARANPOLLYSASHGENTHAPTHYSETLEU 39 SITE	
Sig_peptide 218 . 277	Oy 22SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThr 37 :::	Db 817 TATTATTCTGCATCACAACAACAACAACAACAACCACGGG 861 Qy 101 ProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMet 120	hyta; Embryophyta; Tre opsida; Poales; Poacee glyama,T., Stoll,M. ar eat alpha/beta-gliadir 916 (1985)

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VQQQQFLGQQQPPPPSQQQQQQQQQQQTLQQTLQQQLPYSQPQPFRPQDPY
PQPQYSQPQDPTSQQQQQQQQQQQQQQTLQQTLQQQLTQQQLPYSQQPQPFRPGDPY
SQPLQQYPLGGGSFRPSQQNPQAQGSVQPQQLPQFEEIRNLALQTLPAMCNYTPPYCT
IAPFGIFGTN"
                                                                                                                                                                                                                                                                                                                                                                                                               translation = "MKTFLILVLLAIVATTATTAVRFPVPQLQPQNPSQQLPQEQVPL
                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticae; Triticum.
1. (bases 1 to 3022)
Rafalski, J.A., Scheets, K., Metzler, M., Peterson, D.M., Hedgcoth, C.
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                                                                                                                                                     and Soll,D.G.
Developmentally regulated plant genes: the nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 -----SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu
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117
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743 c 519 g 740 t
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Conservative:
Mismatches:
Indels:
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/db_xref="taxon:4565"
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1591. .1596
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                                                                                                                                                                                                                                                                                                                                                       /product="gliadin"
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/db_xref="G1:21753"
                                                                                                                                                                                   wheat gliadin genomic clone
EMBO J. 3 (6), 1409-1415 (1984)
84261434
                                                                                                                                                                                                                                                                                                                /note="put. TATA-box"
596. .1456
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656. 1453
/product="gliadin"
---="(aa 1-266)"
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/note="putative"
Wheat mRNA for gliadin.

X00627 K03076

X00627.1 G1:21752

gliadin; signal peptide.

Triticum aestivum.

Triticum aestivum.
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TATILICUM aestivum alpha-gliadin storage protein gene, complete cds. U51307
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1 (bases 1 to 3022)
Anderson, O.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (14-MAR-1996) Olin D. Anderson, Western Regional Researc Center, Agricultural Research Service, USDA, 800 Buchanan Street, Albany, CA 94710, USA
Albany, CA 94710, USA
1. 3022
/organism="Triticum aestivum"
                                                                                                                1191
                                                                                                                                                                                            -----TATICIGCAICAACAACAACAACAACAACAACAACAACATCGAGCCAGGT 1239
                                                                                                                                                                                                                                                                        1240 CTCCTTCCAACAGCCTCTGCAACAATA-----TCCATTAGGCCAGGGCTCCTTCCG 1290
                                                                                                                                                       83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn 102
                                                                                                                                                                                                                                   103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
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                                                                         75 -----GluThrAlaCysGlyCysValAla
                                                                                                              1135 ATGGCAGATCCCTGAGCAGTCGCAGGCCATCCACAATGTTGTTCATGCTAT---
                                    1075 ATCACAAGTTTTGCAACAAAGTACTTACCAGCTGTTGCAAGAATTGTGTTGTCAACACCT
60 Ile-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer---
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/clone="CNN54"
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AP003251/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLN 27-APR-1993 clone pW8233,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gliadins, the major wheat seed storage proteins, are encoded by a multigene family and are highly conserved. In the sequence presented here a TATA box is located at positions 492-499 and potential poly-A signals at 1534-1539 and 1591-1596. Four P-boxes (containing many proline codons) are found at 758-793, 794-829, 830-868, and 869-904. The P-box presumably arose in the ancestral alpha/Deta-gliadin gene and was multiplied prior to the extensive multiplication of the whole gene. Every P-box is slightly different from every other. Two polyglutemine stretches reside at 941-994 and 1202-1224. In wheat DNA 'cg' and 'cng' sequences are over 80% methylated to m5c. An alternating purine pyrimidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Summer-Smith, M., Rafalski, J.A., Suglyama, T., Stoll, M. and Soell, D. Conservation and variability of wheat alpha/beta-gliadin genes Nucleic Acids Res. 11, 3905-3916 (1983)

2 (bases 1 to 3022)

Rafalski, J.A., Scheets, K., Metzler, M., Peterson, D.M., Hedgcoth, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                      1240 CTCCTTCCAACAGCCTCTGCAACAATA-----TCCATTAGGCCAGGGCTCCTTCCG 1290
                                          973 ACAACAACAACAACAACAACAATCCTTCAACAAATTTTGCAACAACAACTGATTCCATG 1032
                                                                                                                                 1033 -------CATGGATGTTGTATTGCAGCAACATAGCGCATGGAAG 1074
                                                                                                                                                                                                                        1075 ATCACAAGTTTTGCAACAAGTACTTACCAGCTGTTGCAAGAATTGTGTTGTCAACACCT 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
                                                                                         59
                                                                                                                                                                                   74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wheat (T.aestivum cv. Yamhill) endosperm, cDNA to mRNA, clone pW8233 [2],[3].
----SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrSerLeu 39
                                                                                    40 IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys
                                                                                                                                                                                                                                                                                                             1135 ATGGCAGATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAATGTTGTTCATGCTAT---
                                                                                                                                                                                                                                                                                                                                                            83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn
                                                                                                                                                                                                                                                                   -------GluThrAlaCysGlyCysValAla
                                                                                                                                                                              60 Ile-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] sites; mRNA start, P-boxes.
Sequence in computer-readable form provided by D.Soell,
04-JUL-1985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WHTGLIABE 3022 bp mRNA linear Wheat (T.aestlvum) alpha/beta gliadin class I gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 3022)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete cds.
K03076
K03076.1 GI:170719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soell, D.
Unpublished (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1291 GCCATCTCAGCA 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 ThrValAsnAla 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Soll, D.G.
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JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
JOURNAL
COMMENT
22
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AUTHORS
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PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
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KEYWORDS
SOURCE
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and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APUU3251 149145 bp DNA linear PLN 17-APR-200
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
PAC clone:P0446B05.
stretche with 2-forming potential lies between nucleotides 2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              973 ACAACAACAACAACAACAACAAATCCTTCAACAAATTTTGCAACAACAACTGATTCCATG 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1033 ------CATGGATGTTGTATTGCAGCAACACATAGCAGGATGTTGTAGCAACACATGGAAG 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1135 ATGGCAGATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAATGTTGTTCATGCTAT--- 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 AspLysalaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 -----SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1192 ------TATTCTGCATCAACAACAACAACAACAACAACCATCGAGCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 Ile-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1075 ATCACAAGTTTTGCAACAAGTACTTACCAGCTGTTGCAAGAATTGTGTTGTCAACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 -----GluThrAlaCysGlyCysValAla
                                                                                                                                                                                                                                                                                                                                                  596. .655
/note="alpha/beta-gliadin signal peptide"
656. .1453
/product="alpha/beta-gliadin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3022
36
17
53
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAla--
                                                                                                                                                                     /note="alpha/beta-gliadin precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
                                                                          aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                          /protein_id="AAA34280.1"
/db_xref="G1:170720"
                                                                                                    529. 1626
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596. 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-048-196-2 (1-134) x WHTGLIABE (1-3022)
                                     1. 3022
/organism="Triticum aes/db_xref="taxon:4565"
529. 1606
                                                                                                                                                                                                                                                                                                                                                                                                                                   1021 a 741 c 521 g
1 bp upstream of HindIII site.
                                   Location/Qualifiers
                                                                                                                                                                                         /codon_start=]
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Best Local Similarity:
Query Match:
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us-10-048-196-2.rge

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oin(22593. .23216,24099. .25639,26226. .26367,26499. .26606,
26691. .26903,26990. .27100,27933. .28127,28751. .28925,
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ADTDYLGIPPISQPSNPSFSDINKNYSGLANIRNSTWTRIDGHAEMGRSSTLSTRSYG
KSPTSSNASPGGSPQQHQNIDNINSAFLNYGLGGSPLSPGELPSMMNCMGSGNMPLF
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QYLKAAQSAAQGTANCSDPSLERGFMSSQYGDLTAVQKAYIEALLQQQKQYGMPLGKS
TTSNHGYYGNLAFGMGMAYPGSPLGSPVASPSGPGSPLRLSERNMRFPSNLKNLGGWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="Bab89556.1"
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LVDDXQSHCRRRVPPMPXSSPGLHDALFGLDTIILDDEDEHNSRIMRSNSNMRHNDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSYYYSHGNLNPRLPPPVLSKEDWRSTQRLKAGVVGGIGDGRKVSPEETGHEPTVGRP
YRSONVGFOODEBAARNDVGGAAEWVGGGGGLGIGSLGGGRSFRDLLODNIGRRFPAS
EHPSRAVSRNSFLDNOPGLLXABDSOYSMHNDILEAQRAVGNVQNVSGLPSIRNSASQT
FASVLGSSISRNATPDSHYVPRVPSPGLPPVGVRINSNEKKLNCSSSFWTASSKAVEP
                                                                                                                                                                                                                                                                                                                                                                   ALATEVFTVGGGPPLRAAFGCMATÄFDTSPDGVATAGLLGMNRGALSFVSQASTRRFS
YCISBRDDAGVYLLGHBDLPPLLATPLYQPAPPLPYFDRYNXYVGLLGTRVGGKPL
PTPASVLADPHTGGGTWUNSGTYGFTFLLGDAYSALKAEFSRGTKPRLPALNDDNFAF
OEAFDTCFRVPQGRAPPARLPAVTLLFNGAQMTVAGDRLLYKVPGGRRRGGDGVWCLTF
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VLEHGKPHERSVIIEKLAGQIIQMSQQKFASNVVEKCLTFGGPAEREVLINEMLGTTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENEPLOAMMKDQFGNYVVQKVLĒTCDDQQRELILSRVKVHLSALKKYTVGKHIVARVE
KLVAAGERRIGLQAQYPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MATFSTAGGIGMDASPIWCFMCSRLHRPDGLSTCPTRAPRAALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÉIVEVMDAGEFLÓACALRRAPVAAAVSSTRQQLPTVTVRDAGRTCAVCLDDLEPGGSA
VVTPCDHAYHPQCIAPWLEAHDTCPLCRRESGLQVVEVEVQVDGMVLSSPDGLVLCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMPGGRSEYRLGRRVAGRIFAVRVVDGTGKLVRGGVLRRLGSACHRFAAAAGNLLSLR
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                                                                                                                                                                                                                                                                /translation="mpppppalpyCllLLLLLLLAVPRPAAAAAAATRPLLFELRAR
QVPAGALPRPASKLRFHHNVSLTVSLAVGTPPQNVTMVLDTGSELSWLLCAPGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MGGGGGGGGEGELDELDALLGTGGAGARRRGEDAGERERELNM
FRSGSAPPTIEGSLNAISGLLRGGGEAAVTVAAIPDAETLNGHGGLLSEDELRADPAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEKDMVFKEIMPQALSLMTDVFGNYVVQKFFEHGSAAQRRELADQLFGHVLALSLQMY
                                                                                                                                                                                                                                                                                                                                        GGRSALSFRPRASLTFASVPCDSAQCRSRDLPSPPACDGASKQCRVSLSYADGSSSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(22593. .23216,24099. .25639,26226. .26367,26499. .2
26691. .26903,26990. .27100,27933. .28127,28751. .28925,
29066. .29103)
/gene="PQ446B05.5"
                                      /note="contains EST AU176487(E21047)
similar to Arabidopsis thaliana chromosome 5, At5g02190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNADMVPITAXVICHHHOMNVWEYDLERCRVGLAPIRCDVASERLGLML"
join(13981. .14067,14601. .14684,14736. .14909)
/gene="P0446B05.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jóin(13981. .14067,14601. .14684,14736. .14909)
/gene="P0446B05.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAB89557.1"
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/qene="P0446B05.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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Agrobiotogical Sciences, Rice Genome Research Program: Kannondai
Agrobiotogical Sciences, Rice Genome Research Program: Kannondai
2-1-2, Tsukuba, IDaraki 305-8602, Japan
(E-mail::tasasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
7el:81-298-38-7441, Fax:81-298-38-7469)

On Apr 16, 2002 this sequence version replaced gi:17933036.
Genes were predicted from the integrated results of the following:
GRNSCANI.0, BLASTNZ.0, BLASTNZ.0 as well as SplicePredictor
(October 1998 version). The genomic sequence was searched against
NCBI Nonredundant Protein datebase, nr
(ftp://ncbi.nlm.nth.gov/blast/db) and the CDNA sequence database at
KGP. Protein homologies of the coding regions were searched against
NCBI Nonredundant Protein datebases with BLASTPS.0. ESTS represent
the identified CDNA sequences using BLASTN 2.0 with the
corresponding DDBJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein the indensition program
'unknown' protein. A gene predicted with a gene prediction program
'unknown' protein. A gene predicted with a gene prediction program
significant as a 'hypothetical' protein.
The orientation of the sequence is from SP6 to 77 of the PAC clone.
This sequence of P0446B05 clone has an overlap with P0406G08
(DDBJ:APD01340) clone at the position 1 to 17,095 of 5' end and
with H0005410 (DDBJ:APD0412) at the position 98,039 to 149,145 of
3' end. Detailed information of this entry is available at
http://rgn day affer on inchamcean html
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MAGFTALAACVATYAVASRDPGYPPAFLDDEDAEDPEPHBIKKENDHGIWINNC
VGHRNYKIFLYFVTAVVASLYSLVIVIGAVHSLFRNEDLGSDSSRTSIVSNVOIIC
GVFLCPLALALSILLGWHVYLIFHNKTTIEVHEGVRAMWLAEKAGNLYHHPYDLGVYE
                                                                                                                                         clone:P0446805.
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                              sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains ESTs D23149(C2313),C26277(C12019) similar to Arabidopsis thaliana chromosome 3,At3g09320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(1108. .1218,2391. .2486,2568. .2681,
2756. .2833,2914. .3015,4386. .4661))
/gene="P0446605.1"
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2756. .2833,2914. .3015,4386. .4661))
/gene="P0446B05.1"
                                                                                                                                                                                                                                                                                                                                                                   Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0446B05
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Matsumoto, T. and Yamamoto, K.
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/qene="P0446B05.2"
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complement(11360. .12688)
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/db_xref="G1:20160608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Only in Database (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="P0446B05"
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                                          AP003251.3 GI:20160607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 149145)
Sasaki,T., Matsumoto,T
Direct Submission
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                                                                                                                  Oryza
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ACCESSION
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SOURCE
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AUTHORS
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TAU51306 3034 bp DNA linear PLN 10-APR-1996
Triticum aestivum alpha-giladin storage protein gene, complete cds.
U51306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-MAR-1996) Olin D. Anderson, Western Regional Research Center, Agricultural Research Service, USDA, 800 Buchanan Street, Albany, CA 94710, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnolliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticeae; Triticeae. 1 to 3034)
                                                                                                                           67399
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                                                                                                            uThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuTh
                                                     AATACCCTGTGCACGAACAAAAAGGCTCTCCA-----ACTCCTCTTGCACCATAAAC
                                                                                        rThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThr
                                                                                                                                                                              7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAla----
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36
17
53
41
6
                                                                                                                                                              rLeuLysProCysMetLeuGluThrValAsnAlaPheIleVal 129
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/note="wheat seed storage protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Triticum aestivum"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Cheyenne"
/db_xref="taxon:4565"
/clone="CNN52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                       wheat strain=Cheyenne.
Triticum aestivum
                                                                                                                                                                                                                                                                                                                      U51306.1 GI:1256790
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86.50
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12.80%
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TAU51306
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KEYWORDS
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50835. .51009,51135. .51314)
/gene="P0446B05.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(49471. .49582,49670. .49766,50360...50423,50591. .50619,50835. .51009,51135. .51314)
                                                                                                                                                                                                                                                                                                                                 /Translation="MWMPVDLRLPSGPQAALGILAFEAAAAMSKLLSLHRSLSEGEVS
KLRSDTMRSPGVAYLMSTDAAAAVARLGEKGGIPGGGVA
SLKACAPDARLDPLAKGIRVKAKKHERLVASTARLCSEMEALDELEASERKLAFRGW
NRLSGPIPWQPVAPSAAGDSPGADSLQQDLKAQRIKVRRLKESSLANDGYEKAVGLMA
NRLSGPIPWQPVAPSAAGDSPGADSLQODLKAQRIKVRRLKESSLANDGYEKAVGLMA
DGPSRVHPPVISSSCPIIGLEPSGQVAAIDWRKLLDAPASTVGGAGLDQQANVIVSA
EQLLQMBAEGRQEEANERAEMYEMALDAPASTVGGAGLDQQANVIVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="G1:20160615"
/translation="MLTDLKAIFWTCTGVKQILQDSCGGRRILELGDVAKKGRSWGVG
DVAVAVAAGRWRMLQRGVRRFVNCHAGGTIGPAKMDEKWREREEKTGARKIALCATLF
                                                                                                                       /translation="MTPVSHQLVPPALAAAFGIDLAAVGVLLPSPSVDSPVSHLFFPV
                                                                                                                                      DEDDDEDEEGEGEGGNDDAPAAAAGGGGGRCGKKARNWIPELHHRRYEAVAHLGEK
GAVPKAIVRLMNVDGLTRENVASHLQKYRLYLKRTRVAATPPPSPPPPPPPPPPA
MYVPCFAAKPPLDAANRSDSPPSRTSDATTKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVDRIMAWLGPMARDTVQWQAERNMDRTRRFDGGARVYALQTLRWADKEKAEAALVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /proteIn_id="Bab89562.1"
/db_xref="G1:20160616"
/translation="MTNICAYRARTPNNNSDGPSSKRSRDQPRDRCTHSFSPSGDTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67633
                                                                                                                                                                                                                                                                               /product="putative Avrg/Cf-9 rapidly elicited protein"
/protein_id="BABB9560.1"
/db_xref="G1:20160614"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 SerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(43392. .43820,43852. .43917))
/gene="P0446B05.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(43392, .43820,43852, .43917))
/gene="p0446B05:8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149145
35
19
54
7
                                 /note="contains EST AU082886(C53868)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein"
                                                                                                                                                                                           complement(40152. .41567)
/gene="P0446B05.7"
complement(40152. .41567)
/gene="P0446B05.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                    /protein_id="BAB89559.1"
/db_xref="GI:20160613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'protein_id-"BAB89561.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-048-196-2 (1-134) x AP003251 (1-149145)
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                /gene="P0446B05.6"
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12.87%
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Best Local Similarity:
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RS Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C., Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Bryant, N. P., Burkett, C., Burch, M., Bryant, N. P., Burkett, C., Burch, M., Bryant, N. P., Barbaro, J., Bowte, S. B., Burkett, C., Burch, M., Bryant, N. P., Carrer, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, C., Coyle, M. D., Dathorne, S. R., David, R., Davila, M. L., Davis, C., Davis, C., David, R., Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y. Dinh, H. H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K., Frantz, P., Earnbart, C., Edgart, D., Cawards, C., Elaj, C., Escotto, M., Ralbar, M., Gavara, W., Gunaratne, P., Hale, S., Hamilton, K., Haris, C., Harris, C., Harris, K., Hart, M., Havlak, P., Hames, A., Gant, J., Gavard, J., Garza, H., Holloway, C., Hollins, B., Honsal, F., House, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johsson, R., Johnson, R., Joudah, S., Karlsson, E., Kallson, F., Karlson, R., Ludiet, S., Huber, J., Hulyk, S., Hume, J., Martinez, E., Karlsson, E., Karlson, F., Lucier, A., Lucier, R., Luna, R., Martinez, E., Manhenbari, A., Lucier, A., Lucier, R., Luna, R., Martinez, E., Manhenshari, M., Mapua, P., Matchell, T., Mobbbat, K., Morgan, M., Morson, M., Nouyen, N., Nickerson, B., Mitchell, T., Mobbbat, K., Morgan, M., Nickerson, B., Muchenson, P., Perez, L., Peters, L., Pickerson, R., Potcher, S., Socher, S., Panker, S., Stanley, H., Stone, H., Sutanley, J., Tansey, J., Tanser, S., Varley, Wang, S., Ward-Moore, S., Warren, R., Varley, W., Varley, S., Ward-Moore, S., Warren, R., Varley, W., Varley, S.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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   -----CATGGATGTTGTATTGCAGCAACACATAGT 1074
                                                                                                                           1135 TCAGCACCTATGGCAGATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAATGTTGTTCA 1194
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                                                                         57 TyrTrpLysIle-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIle 73
                                                                                                                                                                                                                               --GluThrAlaCysGly 79
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Rattus norvegicus
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 59 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                               Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 133255) Worley, K.C.
                                                                                                                                                                                 Direct Submission
Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
On Jul 18, 2002 this sequence version replaced gi:20976348.

Center: Baylor College of Medicine
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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Rattus norvegicus clone CH230-262L23, *** SEQUENCING IN PROGRESS ***, 63 unordered pieces.
AC118835 AC118835.4 GI:21747243
HTG: HTGS-PHASE1.
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alibabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarda, J., Benton, J., Biange, K., Blankenburg, K., Bonnin, D., Bouck, J., Borte, P., Brakenburg, K., Bonnin, D., Buhay, C., Burch, P., Burkett, C., Burcell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Dalaney, K. R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisl, A., Gao, J., Garda, A., Garner, T., Garza, N., Gill, R., Gabisl, A., Garcell, J. H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K.,
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hornandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Ja Y., Ohnson, R., Jolivet, S., Joudah, S., Jacobson, B., Ja Y., Johnson, R., Jolivet, S., Joudah, S., Karlsshi, A., Landry, N., Leab, B., Lewis, L.C., Lewis, L., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Lucier, R., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, M., Nguyen, A., Martinez, E., McGod, M.P., Newtson, M., Nguyen, N., Nguyen, A., Martinez, E., McKens, E., Wockenkey, S., Oguh, M., Okwienkey, E., McKens, R., Patch, P., Perez, L., Peters, L., Peters, E., Puble, P., Polie, M., Okwien, G., Soharker, P., Pilms, E., Puble, M., Stone, H., Sutton, A., Warlington, S., Warle, Wang, Q., Wang, S., Warle, Washington, C., Walliams, G., Walliamson, A., Washington, C., Walliams, G., Walliams, G., Walliams, G., Walliams, G., Walliams, G., Mare, R., Washington, C., Wang, S., Warle, M., Y., War, W.Y., Weinston, B., Mang, S., Morley, R., Washington, C., Wang, S., Meres, R., Mashington, C., Wang, S., Marren, R., Washington, C., Walliams, G., Muly, Wuly, Wuly, Wuly, Wuly, Walliams, G., Mulliams, G., Mulliams, G., Mare, M., Y., Walliams, G., Mare, S., Marren, R., Washington, D., Wallish, G., Lander, M., Zorrilla, S., Nelson, D., Weinston, R., Upbula, M., Mang, S., Ware, M., Y., Walliams, G., Mare, M., Wallia, M., Wal
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NOTE: This is a "working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20330712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 185108)
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2: gap of unknown length
7: contig of 1015 bp in length
7: gap of unknown length
8: contig of 1186 bp in length
8: gap of unknown length
9: contig of 1257 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Center project name: GVTY
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Direct Submission
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Arentz-Hansen, E.H.,
Direct Submission
Submitted (05-MAR-1999) Arentz-Hansen E.H., Institute of
Immunology, University of Oslo, Rikshospitalet, N-0027 Oslo, NORWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OQOQOQOQILQQILQQQLIPCRDVVLQQHNIAHGSSQVLQESTYQLVQQLCCQQLMQI
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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Arentz-Hansen, B.H., McAdam, S.N., Molberg, O., Kristiansen, C.
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36.81%
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Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 SerGluSerLysAlaLys-----IleSerGluThrAlaCysGlyCysValAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerLeuIleLysHisAlaVal-------LysGlnThrCysGlnThrGln
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Matches:
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Mismatches:
Indels:
Gaps:
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Best Local Similarity:
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                                                                                                                                  PAT 20-JUN-2002
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1129 GCATAAGCCGCAATAGCCGCAGCGGGATGCTTTTGACTGGCCTTGCTTAAGTATTCCAGG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified.

1 (bases 1 to 3823)

1 batenty,F.W. burland,V., Perna,N.T., Plunkett,G. and Welch,R. Sequences of E. coll 0157

Patent: US 6365723-A 132 02-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1402 GAAGGAACTGGAAGCACTGGAAGATCAAACACAGGCGTATTTTTCTTTTTTCTCTTTGTC 1343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 AlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArg 104
                          600 CTCCTTCCAACAGCCTCAGCAACAATA-----TCCATCAGGCCAGGGCTTTTTCCA 650
103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 LeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 LysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 GluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 ThrGluValAlaGlnLysIleValArgHisSerLeuLysProCys-------
                                                                                                                                   linear
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22
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29
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Conservative:
Mismatches:
                                                                                                                                AR204236 3823 bp DN
Sequence 132 from patent US 6365723.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AlaPheIleValProThrThrArg 134
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  /organism="unknown"
961 c 900 g
                                                                                                                                                         AR204236.1 GI:21500834
                                                                                                                                                                                                                                                                                                                                                                                    57.1
85.50
36.91%
22.15%
12.65%
                                                   ThrValAsnAla 126
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| 651 ACCATTTCAGCA 662
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Best Local Similarity:
Query Match:
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AE005438/c
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KEYWORDS
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                                                                                                       RESULT 37
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AELQRRILDNQQTGSAQSDAALLWSFWNSYSADELVDDLVIRGGLESAVEIVLFALQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carriers: Molybdopterin" hote-"Residues 1 to 218 of 242 are 37.75 pct identical to residues 1 to 244 of 274 from Escherichia coli K-12 Strain MG1655: B2115"
AE005438 . . 11010 bp DNA linear BCT 21-MAR-2001
Escherichia coli 0157:H7 EDL933 genome, contig 3 of 3, section 57
of 290.
AE005438 AE005174
AE005438.1 GI:12516330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulator; Biosynthesis of cofactors,
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//note="O-island #90; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655"
1019. .3910
                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,
Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A.,
Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L.,
Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K.,
Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
Welch, R.A., and Blattner, F.R.
                                                                                                                                                                                                                                                                                                             l (bases 1 to 11010)
Pernah NT., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Kilnk, S., Boutin, A., Shao, Y., Miller, L., Grotbacck, E.J., Davis, M.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
Nature 409 (6819), 529-533 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-CCT-2000) Laboratory of Genetics, Ur
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /serotype="0157:H7"
/db_xref="taxon:155864"
/note="enterohemorrhagic"
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                                                                                                                                                                                        Escherichia coli 0157:H7 EDL933.
Escherichia coli 0157:H7 EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101. .829
/gene="molR_A"
/note="Z3283"
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/note="Z3284"
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/gene="molR_A"
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/transl_table=11

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/ LEGISLAGORGKENITWINYDKCSLEWGSAIQOAINLIGEHKPSIPALTGSLIQ
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NDSQOLLDEIVOGEGERATPUVISROCIARRE ESDSLUVTLOGODOSTGGGSGATY
NDPOLLERWHISLAEESCWORCADKLIAALOSIRKIREDFIALIDEKPETANELASL
ESSRSSLHSKEWLKVVATDNITAVKKLERYWGLDVFSDREASYMSQENREGYAACASLL
REGGLAAVPRLAANYAHKEDGOSLLVOINHOVYTRTLLIADANNKPSLQRAAKYSKNEP
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VMSWLSTQARAVLKSYLSALPKPVIDGTDNSNLPEILVSPPWRSKKKMTAPRLDLARL
ELTPOVYWQPGERRELAATESARYESTESLAQREGKSGRVVLQELGFGDDVWLELNY
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LAFSHRPKETFPLILNFGATELALPWARVWRRFAAQNELARGATATALIDL
VFTKSSDSKSFAALLALRLYFWLENGTGELLOYNNRPEAGOLAFCOG
RIPKAADPFWHHQWMSRPRITTNNQPVTDDALEIIGEMLKFTGGGFFYSGLEGLKTFCO
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PTLGLDDPQALSFDFGPRQFTVRFDENLNPVIFDQQNVRQKSVPRLRADDDQLKAPEA
LARLKGLKKDATQVSKNLLPRLEAALRTTRRWSLADFHSLFVNHPFTRLVTQRLIWGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="orf; Unknown function"
/note="Residues 1 to 105 of 105 are 99.04 pct identical to
residues 1 to 105 of 105 from GenPept 118 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAG$7181.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPANEPRRLLNAFRVAAEGGFCNAQDEPIDLPADALIGIAHPLEMTAEMRSEFAQLRA
DYEIMPPFRQLARRIVLLTPDESTSNSLTRWEGKSATVGQLMGMRYKGWESGYEDAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gi|405847|gb|AAA60479.1| (U00007) yehK [Escherichia coli]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDLGEYRLVLKFSPGFNHYNVDSKALMSFRSLRVYRDNKSVTFAELDVFNLSEALSAP
                             /function="putative regulator; Not classified"
//note="Residues 1 to 1209 of 1209 are 94.04 pct identical
to residues 1 to 1210 of 1210 from Escherichia coli K-12
Strain MG1655: B2118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="0-island #91; Region of the EDL933 chromosome not
homologous to E. coli K-12 MG1655"
2709 c 2653 g 2631 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrValThrAlaThrLeuMetThrAlaPhe---ThrLeuAlaSerCysAlaSerThrPro
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Conservative:
Mismatches:
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/db_xref="GI:12516335"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVIFH"
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/note="z3288"
10609. 10926
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Best Local Similarity:
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                                                                                    /translation="MTWLRLVITDDTALSTVEKYDFPPLYRDFRNFRAYLAMLLANNG
YGVSRILLEFTEDHSONPTYLEREISETENLYKWLMKTNHPDAIQILLIGVICKKKH
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GILSECRPQSVAEECEYATVDMLPELLVSPPWMTKEKKKNTPVFDLPVLEVPSYSDYT
                                                                                                                                                                                                          PEITKKLTRTYLVTHFQOIAQOQATKQTLFTDLPPIKKASWEKHLIPLTPEGOILWHL
GEKURESGEKLYEK IPAPGOSAVDALLEREPFPALNAEFWYHNINAYKESWILIALCYLD
GQQA ISFLNOI VKENDYSGEONILA IFGSAAIPAFWACLQRDPRRLCEFPFFLGVSEL
ALPMAQQLQKKMSYEDDARWLTDYPRHAAAGLLPVALGKKGRORDCARQALRLLVNLN
GRET EEBIAGOGVNQPDVLAALATTENSDPLEBYPAK IAPLEGFYOFTURRRPRLKSNN
LPLSDDAMRHLGTMAFSPRDITAYAGLDITREIFTRESLAEFGWDLYPAWTEAGAPAK
ENWAFTSLGILGNDDTARKLTPLIRAWGESOHKRAVSGLDVLADIGSDVALMLLNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                  ARKIKFKALQEHAREKINIVAENRGITMAELEDRLAPDIGLDSSGSLILDFGPRKFTV
GFDETLKPVVCDANGKVLKDLPKPNQSDEKTQATDAVNLFKQLKKDVRAIASQQIDRL
EQAMCQRRRWTAEQFRLFLVEHPLVRHLTRRLLMGVYNDENALITCFRVAEDSTYSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSCSDEWADAISQAISLIKAOKTEIPARTWAVLTFLEICFCQGWNDETSSELLDEIVS
TFGIEXATETVIFWOIDFDPDYKDBHLTFFINYADSSKDSYRRNUNKFSLERKKHLS
LAGEEVWQNCIAKLLVALDDISLYROPLIAILMPEIPEVAHEIVHRLHOVADVPQLEM
LKLVATDPFTLEILENYQYIDVFNYGASWSATVLREQGIAALARLTPYAEEDNCGDV
LKCINHPLAIINKKCRKFSFCNDSGISRSIGKKR"
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PLWTRPKLKNSSNVLPDSALCHLGEMARFOGEALYFGLLQVKDACTADSLAFFANDL
FTAMLTAGAPSKESMAFTALGVLGNDDTARKLTPLIRAWPGESQHKRATVGLDILAAI
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LLLDFGSRQFTVSFDETLKPFVRDVSGSRLKDLPKPNKSDDESQANDAVNRYKLLKKD
ARTVAAQQVARLESAMCLRRRWSPENFQLFLVEHPLVRHLTRRLIWGVYSTENQLLTC
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DRNSYALTEAERNASELTRWAGRKCPSGRVWGLANKGWIKGTPQDGGWIGWMIKPLGR
WSLIMEIDEGFAVGMSPAELSAEQILSKLWLWEGXAESYGWGSNSTQEAQFSVLDAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HELTRWQGRLCQAGRIYGLERRGWQRLEESGSYYAMRKTTPHGDLELETEPFSLIYGE
TGYGDQHPVESYKITSPDDRYGKQSSLTFSMLDDITASELINDIESLFD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKTYIYQDEKSHKFWAVEQQGNELHINWGKVGTNGQSQVKSFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAAEKAALKLIAEKVKKGYVEQVDANAHSHDASAKKVLVTEEKASTNRQAATNGLPW
LADNDPIILPPNIARHALSHRLWPGEPVKKPTKPEKQNLISRLANRTYHYYKNLTFDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDELFTLPAGNIGIPHVLEISPESAAAFRQIYADYELLPPFQQLERGSYHLADNERNT
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Ante-Residues 100 to 402 of 426 are 43.03 pct identical

to residues 5 to 309 of 1210 from Escherichia coli K-12

Strain MG1655: B2118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Residues 1255 to 579 of 579 are 94.92 pct identical to residues 19 to 333 of 333 from Escherichia coli K-12 Strain MG1655: B2117"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function-"putative regulator; Biosynthesis of cofactors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function-"putative regulator; Biosynthesis of cofactors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"putative regulator (fragment)"
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regulator (fragment)"
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/note="23285"
3923. .5203
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/gene="yeh1"
/note="23287"
6918. .10547
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AC124403 243098 bp DNA linear HTG 20-JUN-2002 Mus musculus chromosome UNK clone RP24-36916, WORKING DRAFT SEQUENCE, 10 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49807 TTTGTCTGTATAGCA-----CCTGTCCCAGTTGTTTCCTACTGTCACCTTGATTCAAGA 49754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHis 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 TrpLyslleAlaAlaMetLysLeuSerSerGluSerLysAlaLyslleSerGluThrAla 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 CysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAla
soon as it is available and the accession number will
                                    contig of 1149 bp in length
contig of unknown length
contig of 3187 bp in length
day of unknown length
contig of 6192 bp in length
gap of unknown length
contig of 11841 bp in length
gap of unknown length
contig of 11841 bp in length
contig of 11841 bp in length
                                                                                                                                                                                                                      34810: gap of unknown length
157377: contig of 122567 bp in length
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AC124403.1 GI:21426522
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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/537. .10728

/note-"assembly_name:Contigl3"

/note-"assembly_name:Contigl4"

22770. .34710

/note-"assembly_name:Contigl4"
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Mismatches:
Indels:
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. 34599 c 36427 g 43883 t
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Matches:
                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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/chromosome="UNK"
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                                                                                                                                                                                                                                                                                                                                                                   /clone="RP24-326N11"
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                   10728:
10828:
22669:
22769:
34710:
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as soon as it
be preserved
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Best Local Similarity:
Query Match:
                                                         1150
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KEYWORDS
SOURCE
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Direct Submission
Submitted (05-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 157377)
MCPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                 1443 GTAATCAGTTTGACAAGCGCTTTACGCCACTCTTTATCTTCATGTATTGCCAGCAAAGTA 1384
                                                                                                                                                                                                                                                                                                                                              1383 GCATAAGCCGCAATAGCCGCAGCGGGATGCTTTTGACTGGCCTTGCTTAAGTATTCCAGG 1324
                                                                                                                                      85 AlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArg 104
                                                       65 LeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys
                                                                                                                                                                                                                                                                                                       -------MetLeuGluThrValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 178000; agarose-fp
Insert size: 158206; sum-of-contigs
Quality coverage: 13.54 in 020 bases; agarose-fp
Quality coverage: 13.67 in 020 bases; sum-of-contigs
                                                                                                                                                                                                               105 ThrGluValAlaGlnLysIleValArgHisSerLeuLysProCys-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid: 1008
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 156063 bases at least 030
Consensus quality: 156047 bases at least 030
Consensus quality: 157390 bases at least 020
              1596 ATCCAGGGCGGCGAACAAGCAGCTCCGGCAAC-
                                                                                                                                                                                                                                                                                                                                                                                                                1323 TGCTTTTCTTACCAATTACACCGAGG 1297
                                                                                                                                                                                                                                                                                                                                                                                    126 AlaPheIleValProThrThrArg 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC123926.1 GI:21326382
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
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                                                                                                                                                     Therefore 1 to 243098)
MCPherson, J. D. and Waterston, R. H.
Bulrect Submission
Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 243098)
MCPherson, J. D. and Waterston, R. H.
                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 243098) McPherson, J.D. and Waterston, R.H. The sequence of Mus musculus clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 238434 bases at least Q40
Consensus quality: 238425 bases at least Q30
Consensus quality: 238425 bases at least Q30
Insert size: 178000; agarose-fp
Insert size: 242198; sum-of-contigs
Quality coverage: 17.40 in Q20 bases; agarose-fp
quality coverage: 10.31 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of unknown length contig of 107231 bp in length app of unknown length contig of 83148 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 4893 bp in length
gap of unknown length
contig of 12030 bp in length
gap of unknown length
contig of 12206 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 1312 bp in length
gap of unknown length
contig of 1105 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 14283 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...... Summary Statistics
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8823: gap of unknown length
6090: contig of 2267 bp in length
6190: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
of 4893 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Db 145256 GGTTAGACGGTCTCTCTCTCATTCTGCTTCAGCATAAGTTGGGGCCACAGGTGACACTGCA 145315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysH1s 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 TrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGlนี้ThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 AlaValLysGlnThrCysGlnThr-------GlnLeuThrGlyHisGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 CysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAla
                                                                                                                                                                                                                                                                                                                                                901 others
                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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6191. .11083
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157334, 240481
/note="assembly_name:Contig17"
240582, 241893
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241994. .243098
/note="assembly_name:Contig9"
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56705 c 54885 g 64824 t
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Best Local Similarity:
Query Match:
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Job time: 2107 secs
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٠,; 40 Sequence 7, April Sequence 15, April Sequence 15, April Sequence 19, April Sequence 1, April Sequence 2, April Sequence 21, April Sequence 11, April Sequence 12, April Sequence 12, April Sequence 1, April Seque

Scoring table:

Searched:

Minimum

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Run on:

Appli Appli

Sequence 1, Al Sequence 1, Al Sequence 31, Al Sequence 31, Al Sequence 31, Al Sequence 31, Al Sequence 263, Al

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US-08-961-527-28/c

Sequence 28, Application US/08961527

Patent No. 6420135

Patent No. 6420135

Patent No. 6420135

Patent INPERMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCE: 391

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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US-09-658-655-71
US-09-658-655-71
US-09-125-642C-8
US-09-125-642C-12
US-09-125-642C-12
US-09-125-642C-12
US-08-309-420-1
                                                                                               .05-09-370-838-152

.05-09-370-838-152

US-09-660-756-98

US-08-632-598-1

US-09-121-240-1

US-09-125-642C-3

US-09-255-829-28
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US-08-961-527-263
                                                                     JS-08-001-554A-7
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 9B340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5258502-1
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                439
1712
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1080
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                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Maryland
COUNTRY: USA
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-DB-Issued_Patents_NA -OFMT=fastap -SUFFIX-rni -MINMATCH-0 1 -LOOPCL-0
-LOOPEXT-0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST-45 -DGOCALIGN=200 -THR_SCORE-Epct -THR_MAX=100 -TRR_MIN-0 -ALIGN=40
-USER-US10048196_eCGN_11_32_erunat_28042003_151440_5608 -NGPU=6 -ICPU-3
-NODEL-LOOAL -OUNFWT-P1O -NORM-ext -HEAPSTEE=500 -MINLEN-0 -MAXLEN-200000000
-USER-US10048196_eCGN_11_32_erunat_28042003_151440_5608 -NCPU=6 -ICPU-3
-NO.MMAP -LARGEOGERY -NGC_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -YGAPOP=6 -FGAPOP=6 -DELEXT=7
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1 MMKILXVTATLMTAFTLASC.....SLKPCMLETVNAFIVPTTTR
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                              5.1.4_p5_4578
Compugen Ltd.
                                                                                                                                                                            nucleic search, using frame_plus_p2n model
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US-09-453-702B-132
US-09-724-864-21
US-08-817-942C-1
US-08-818-189D-28
US-08-852-344D-28
US-08-852-344D-28
US-08-467-963C-7
US-08-467-963C-7
US-08-838-189D-7
US-08-852-344-07
US-08-852-344-07
US-08-852-344-07
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                              GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
Sequence:
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888.5 85.5 77 77 76.5 76.5 76.5 76.5 76.5

Score

Result

Database

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                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                          58 TrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAla---LysIleSerGluThr 76
                                                                                                                                                                                                                                                                                                                                                                                                                77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGlu-----Leu
                                                                                                                                                                                                                                                                  5016 AATGAAAATGATAACCTTACGTCCAAGCAAATTAAATTCATAGATGCCATGCTTACCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                               4836 ACAACTCAAATGCTTTATTTAGCATCATCTAACGCTGTTTCTGTACTCAATGATATTATG
                                                                                                                                                                                                                                                                                                 43 ---AlaValLysGlnThrCysGln------ThrGlnLeuThrGlyHisGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Welch, Rod TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.50 inch. 1.44Mb storage
                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                        30 AsnSerSerAlaAsnLeuThrThrSerLeuIleLysHis---
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FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Blattner, Frederick R. Burland, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 132, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Seay, Nicholas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicole T
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Perna, Nice
Plunkett, Guy
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5857 base pairs
                                                                                                    0.747
88.50
48.54%
27.18%
13.09%
               nucleic acid
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                                            linear
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                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                 TYPE: nucleic
STRANDEDNESS:
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                                           ; TOPOLOGY:
US-08-961-527-28
                                                                                      Alignment Scores:
 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Watson, James D
APPLICANT: Wartson, James G.
TITLE OF INVENTION: POLynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysGlnThrCysGlnThrGlnLeuThrGlyH1sGlnTyrTrpLysIleAlaAlaMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 AlaproGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-048-196-2 (1-134) x US-09-453-702B-132 (1-3823)
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                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                            Indels:
Gaps:
                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 132:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILLING DATE: 2007.11 20 PRIOR APPLICATION UNBER: U.S. No. 6380362 PRIOR FILLING DATE: 1999-12-23 NUMBER OF SEQ ID NOS: 72 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/724,864 CURRENT FILING DATE: 2000-11-28
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
                                        TELEFAX: (608) 251-91
INFORMATION FOR SEQ ID NO: 132
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      0.94
85.50
36.91%
22.15%
12.65%
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Best Local Similarity:
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US-09-724-864-21
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2045 ACTTAGGAGCGGAGTACATGCAATCTGTCGGTAACATGAGGAAGTGCTCAACCTCACGAC 2104
                                                                                                                                                                                                                                                                                                                                44 -----ValLysGlnThrCysGlnThrGlnLeuThr------GlyHisGln 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 TyrTrpLys1leAlaAlaMetLysLeuSerSerGluSerLysAlaLys1leSerGluThr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                          12 MetThralaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSer 31
                                                                                                                                                                                                                                                                                                                                                                                        ----IleLysHisAla----
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APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEMART, KOLASCH & BIRCH, LLP
STRRET: P.O. 500X 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2210 TCATGCCCTGAGGGTTGGGGCTAACTGGTGTAGTCTTCGCTGCTGTG 2257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                     US-10-048-196-2 (1-134) x US-09-724-864-21 (1-2324)
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FILING DATE: 09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08387942C Patent No. 5939289
                                                                                                                                                                                                                                                                                                                                                                                      32 SerAlaAsnLeuThrThrSerLeu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MRRHY JR. GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2105 TCCTGGAAGCCTGCACTT-----
                                                                                                                                  5.41
77.00
37.93%
23.28%
11.39%
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                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                  TYPE: DNA
CRGANISM: Mouse
US-09-724-864-21
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                                                                                                                  Alignment Scores:
SEQ ID NO 21
LENGTH: 2324
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                                                                                                                                  red. No.:
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APPLICANT: DU, Run-Pan
APPLICANT: EMASYSSHYN, MARY
ETPLICANT: EMASYSSHYN, MARY
TITLE OF INVENTION: CHIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ANDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 11525 ACGGCAACTTCGTCGCCGCTTCAACGATGCCAACCTGTTGTTCGACGCCGCTCCGGTCA 11584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 ProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThr 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 CysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSer 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 ThralaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsn 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 11789 GCGACAACCAGGGCGATTACATCATCGACTTCGCCGTGGGCGAAGAA 11836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-048-196-2 (1-134) x US-08-387-942C-1 (1-12588)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
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                                                                                                                                                                                                               ORGANISM: Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/08467963C
Patent No. 5968776
GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12588 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.21%
25.86%
11.39%
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9973..12588
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2227..6438
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6702..9695
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Best Local Similarity:
                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                     STRAIN: E
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US-08-467-963C-28
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NAME/KEY:
LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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; LOCATION:
US-08-387-942C-1
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PACENT NO. 5998169
GENERAL INCORNATION:
APPLICANT: KLEIN Michel H
APPLICANT: KLEIN Michel H
APPLICANT: BUASYSHYN, Mary E
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 ATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATATTCATAGCCTCG 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle 40
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      --AACCACAAACAAACCCAATAATGATTTTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
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Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-048-196-2 (1-134) x US-08-838-189D-28 (1-894)
                                                                                                                                                                                                                                                                                                                                                       E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                             3, Application US/08838189D
5998169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (416) 595-1163
INFORMATION FOR SEO ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.44%
25.00%
11.32%
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                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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CLASSIFICATION:
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Best Local Similarity:
Query Match:
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STREET: 6t
                                                                 RESULT 6
US-08-838-189D-28
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                                                                                                                 ; Sequence 28,
                           461
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                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/467,963C
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION UNDER: US 08/838,189
APPLICATION NUMBER: US 08/838,189
FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-474 MIS:jb
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION SEQ. 1163
INFORMATION FOR SEQ. 1D NG: 28:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-048-196-2 (1-134) x US-08-467-963C-28 (1-894)
3: Sim & McBurney
6th Floor, 330 University Avenue
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                  STREET: 6th Floor, 330 Univers
CITY: Toronto
STATE: Ontario
COUNTX: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.44%
25.00%
11.32%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
Query Match:
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US-08-467-963C-28
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                                                                                                                          349 TCAACAACACCCAGGAGTCAAGTCAAACCTGCAACCCACAACAGTCAAGACTAAAAAACACA 408
58 TrpLyslleAlaAlaMetLysLeuSer-----SerGluSerLysAlaLyslleSer
                                                                                 75 GluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeu
                                                                                                                                                                    ThrThrAlaAlaIle-AsnPro-------AsnAlaArgThrGluValAl
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KLEIN, Michel H
APPLICANT: DU, Run-Pan
APPLICANT: DU, Run-Pan
APPLICANT: EWASYSHYN, Mary
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            108 aGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThr 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
BELLCATION NUMBER: US/08/852,344D
FILING DATE: 07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-688 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
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APPLICATION NUMBER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          US-08-852-344D-28
; Sequence 28, Application US/08852344D
; Patent No. 6017539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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25.00%
11.32%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Toronto
STATE: Ontario
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
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-----AsnAlaArgThrGluValAl 108
                                                                                         133 ATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATATTCATAGCCTCG 192
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                                                                                                                                     21 AlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle 40
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                                            1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
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APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 -------AACCACCAAACAAACAAACAATGATTTTCACT 493
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,639E
FILING DATE: 14-NOV-1994
CLASSIFICATION: 424
PROF.
US-10-048-196-2 (1-134) x US-08-852-344D-28 (1-894)
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330 University Avenue, 6th Floor
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REFERENCE/DOCKET NUMBER: 1038-391 MIS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-344-639E-28
; Sequence 28, Application US/08344639E
; Tactent No. 6033668
; GENERAL INFORMATION:
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ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                              US-10-048-196-2 (1-134) x US-08-344-639E-28 (1-894)
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Indels:
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STREET: 6th Floor, 330 University Avenue
CITY: Toronto
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APPLICANT: DV, RUN-PAN
APPLICANT: BMS, SHY, EMASY E
TITLE OF INVENTION: MULTIMERIC HYBRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 7, Application US/08467963C
Patent No. 5968776
             TELEX: 065-24567 SIMBAS INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
(416) 595-1163
                                                                    LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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76.50
40.44%
25.00%
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TITLE OF INVENTION:
TITLE OF INVENTION:
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COUNTRY: Canada
ZIP: M5G 1R7
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Best Local Similarity:
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TELEFAX:
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DB:
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140 ATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATATTCATAGCCTCG 199
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416 ACAACCAAACCCAAACCCAGCAAGCCCACTACAAAACAAGCCCAAAAACA-
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APPLICANT: KLEIN, Michel H
APPLICANT: DU, RUn-Pan
APPLICANT: EMASYSHYN, Mary E
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING.
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34
21
23
53
53
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Mismatches:
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                                                                                                                                                                                                                                                                         NAME: STEWART, Michael I
REGISTRARION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-474 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
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APPLICATION NUMBER: US/08/467,963C
                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,189
FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08/001,554
                                                                                                                         APPLICATION NUMBER: US 08/001,55.
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTONEY/ASENT INPORMATION:
NAME: CEMESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08838189D Patent No. 5998169
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.44%
25.00%
11.32%
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Best Local Similarity:
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US-08-838-189D-7
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No
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108 aGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThr 123
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 101
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: MSG IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                              Toronto
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CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS 38
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140 ATTCTGGCAATGATAATCTCCACTTTCATAATTACAGCCATCATATTCATAGCCTCG 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 GluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeu 94
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                        ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1038-687 MIS: jb
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APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-11
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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25.00%
11.32%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCE
                                                   NUMBER OF SEQUENCES:
            INVENTION:
                                                                                                                                                     STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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US-08-838-189D-7
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                                                                                                            APPLICANT: DU, RUD-Pan
APPLICANT: EWASYGHYN, MARY E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 37
NUMBER OF SEQUENCES: 37
ADDRESSEE: SIM & MCBURNEY
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,344D
FILING DATE: 07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
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Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION NUMBER: GB 9200117.1.
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
Sequence 7, Application US/08852344D Patent No. 6017539 GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
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236 CANGATCGAACCAATCAACCAACCAATCAGGACCCAACTCAGG 295 29 STEPLYSIICHIAAIABALBELUSIEUGE. 74 29 STEPLYSIICHIAAIABALBELUSIEUGE. 74 29 CTTCGAATCACCCCCCAATCATCGTCTGATCATCATCATCATCATCATCATCATCATCATCATCATCA	Pred. No.	Percent 3	Best Loca	DB:	US-10-048	γo	Db 140	0y 21	DP 200	Qy 41	Db 236	0y 58	962 qa	Oy 75	Db 356	96 VQ 95	Db 416	00 108			RESULT 13 US-08-467	; Sequenc ; Patent	GENERA SPE	APPL	TIT.	COR				~ S	# C		COL	.;	CL CL	A		. AP	
- 0 0 0 0 0 0 0 0 0 0 Mbaaaaaaaaaaaaaaaaa	:::		58 TrpLys1leAlaMetLysLeuSerSerGluSerLysAlaLys1leSer ::::	296 CTTGGAATCAGCTTCTCCAATCTGTGTAAATTACATCACAAACCACCACACATACTAGCT	75 GluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeu	356 TCAACAACACCAGGAGTCAAGTCAAACCTGCAACCCACAACAGTCAAGACTAAAAAACACA	95 ThrThrAlaAlaIle-AsnProAsnAlaArgThrGluValAl	416 ACAACAACCCAAACCAACCAGCAGCCCACTACAAAACAACGCCAAAACAA	108 aGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThr	468AACCACCAAACAAACCAATAATGATTTCACT	ESULT 12 '- E-08-344-630E-7	Sequence 7. Application US/08344639E Datent NO 6033668	GENERAL INFORMATION: ADDITION: Michel H	APPLICANT: Du, Run-Pan			CORRESPONDENCE ADDRESS:	SSEE: Sim & McBurney F: 330 University Avenue,	Ē.,	PRY:	ZIP: M5G IR7 COMPUTER READABLE FORM:	COMPUTER: IBM PC compatible	OS/MS-DOS ease #1.0, Version #1	708/344.639E	FILING DATE: 14-NOV-1994	PRIOR APPLICATION DATA:	APPLICATION NUMBER: US 08/001,554 FILING DATE: 06-JAN-1993	CLASSIFICATION: 424 PRIOR APPLICATION DATA:	APPLICATION NUMBER: GB 9200117.1	CLASSIFICATION: 424	ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I	STRATION NUMBER: 24,973 SENCE/DOCKET NIMBER: 1038-391	1	TELEFAUNE: (416) 595-1155 TELEFAX: (416) 595-1163	TELEX: U55-2456/ SIMBAS INFORMATION FOR SEQ ID NO: 7:	SEQUENCE CHARACTERISTICS: LENGTH: 920 base bairs	r E	inear	-639E-7

Alignment Scores:

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0 ATTCTGGCAATGATATCTCAACTTCACTTATAATTACAGCCATCATATTCATAGCCTCG 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys 20
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CULTY: TOTONCO
COUNTY: Canada
ZIE: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORY
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,969A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-ANN-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-ANN-1993
CLASSIFICATION: 435
ATTONEY AGENT! MICHAEL 17
NAME: ASSIFICATION: 435
ATTONEY AGENT! MICHAEL 17
920
34
21
23
28
53
Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                              Similarity:
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67-969A-7
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355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
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Matches:
Conservative:
Mismatches:
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                           1038-475 MIS:bh
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330 University Avenue, 6TH Floor
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Patent No. 6171703
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038

TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1165

TELERAX: (416) 595-1163

TELERATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Du, Run-Pan
APPLICANT: Bwasyshyn, Mary E
TITLE OF INVENTION: Chimeric
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                   ; MOLECULE TYPE: DNA (genomic)
US-08-467-969A-7
                                                                                                                                                                                                                                                                                                                                                      76.50
40.44%
25.00%
11.32%
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ADDRESSEE: Sim & MCE
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
DB:
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STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                Alignment Scores:
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US-08-467-961A-7
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CITY: TO
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140 ATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATATTCATAGCCTCG 199
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34
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             PatentIn Release #1.0, Version #1.25
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-048-196-2 (1-134) x US-08-467-961A-7 (1-920)
                                                                                                                                                                                                                                                                                                                                                              1038-476 MIS:bh
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Matches:
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SOFTWARE: Palence.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,961A
                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELES: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Query Match:
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 ATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATATTCATAGCCTCG 199
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Mismatches:
Indels:
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                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                   APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Dwasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
TUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,554A
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-286
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    COMPUTER FEADMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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TELEFAX: (416) 595-1163
TELEEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                  Klein, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.5
76.50
40.44%
25.00%
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TYPE: nucleic acid
STRANDEDNESS: single
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GENERAL INFORMATION:
                                                                                                                                                                                       COUNTRY: Canada
ZIP: M5G 1R7
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Best Local Similarity:
Query Match:
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1426 TTGAGGAAGTICTTCTTTCTCAGAGCTACGTTAAAATGTATAACAAAGCTGTCAAGCTGT 1485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 ----- AsnProLysAsnSerSerAlaAsnLeuThrThr------Ser-LeuIleLy 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 lyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 sHisAlaValLys-----GlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLy
                                                                                                                                                                                                                                                                                              APPLICANT: Modemath, Roadel APPLICANT: Secrist, Heather APPLICANT: Secrist, Heather TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF 1 TITLE OF INVENTION: COMPOUNDS FOR THEIR USE FILE REFERENCE: 210121.475C1 CURRENT APPLICATION NUMBER: US/09/370,838 CURRENT FILING DATE: 1999-08-09; EARLIER FILING DATE: 1999-08-09; EARLIER FILING DATE: 1999-04-02; NUMBER OF SEQ ID NOS: 289; SOFTWARE: FEALSEQ for Windows Version 3.0
                                  ---AACCACCAAACCAATAATGATTTTCACT 500
108 aGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThr
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         indels:
                                                                                                                                                               ; Sequence 152, Application US/09370838; Patent No. 6444425
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US-09-351-200-1
; Sequence 1, Application US/09351200
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76.50
40.918
25.328
11.328
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                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                        US-09-370-838-152
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Alignment Scores
                                                                                                                                                                    LENGTH: 439
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1685 GCTACAAGCAGCTCCTCAACTTTTATTAGAACTGCTTCCATTAATGGTTTT 1744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 GluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsn 125
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APPLICANT: BOURBONNAIS, YVes
APPLICANT: LAWARE, Claude
APPLICANT: LAWARE, Claude
TITLE OF INVENTION: CANDIDA ALBICANS GENE (CSA1) ENCODING A
TITLE OF INVENTION: MYCELIAL SURFACE ANTIGEN, AND USES THEREOF
FILE REFERENCE: 6013-71"US" CC/
CURRENT APPLICATION NUMBER: US/09/351,200
CURRENT APPLICATION NUMBER: CA2,237,134
EARLIER APPLICATION NUMBER: CA2,237,134
SEALIER PILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
EMEGTH: A291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
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Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us-09-060-756-98
; Sequence 98, Application US/09060756
; Petent No. 6183957
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2015 GCTACTGCAGTACCAACCTCC 2035
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75.00
41.50%
24.49%
11.09%
                                                                                                                                                                                                                                                                                                           ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: gene
; LOCATION: (0)...(0)
US-09-351-200-1
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                          TYPE: DNA
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No.
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APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEC ID NOS: 743
SOFTWARE: PALGULIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GCCACCCTGGCCGAAAGCTCGACA 424
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Sequence 1, Application US/08632598
Sequence 1, Application US/08632598
Sequence 1, Application US/08632598
Sequence 1, S88164
GENERAL INFORMATION:
APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  439
24
17
38
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,598
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
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                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-060-756-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,7
                                                                                                                                                                                                                                                                                                                                                                                     74.00
48.24$
28.24$
10.95$
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425 TGGTCAATCCGGCCG 439
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                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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CURRENT APPLICATION DATA
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APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   1712
28
26
43
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
223355/SEE50112/US
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CUSHMAN DARBY AND CUSHMAN STREET: 1100 NEW YORK AVENUE N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA ZIP: 20005-3918
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         TELECOMANCE: No. TELEPHONE: No. TELEPA: 822-0944
TELEX: 6714627 CUSH
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
              TELECOMMUNICATION INFORMATION: TELEPHONE: 861-3000
REFERENCE/DOCKET NUMBER:
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26.67%
10.95%
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STRANDEDNESS: sli
TOPOLOGY: linear
MOLECULE TYPE: CDN
ORIGINAL SOURCE:
ORGANISM: MUSA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                               ACS GENE
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Query Match:
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Sequence 3, Application US/09125642C
Patent No. 6365393
GENERAL INFORMATION:
APPLICANT: BAYER AG
TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
Their Production and Their Use in Vaccines
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Matches:
Conservative:
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Indels:
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ADDRESSEE: Bayer Corporation
US/09/231,240
                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 22:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 861-3000
                                                                                                                                                                                                                                                                       TELEFAX: 822-0944
TELEEX: 6714627 CUSH
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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51.43%
26.67%
10.95%
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    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: MUSA
IMMEDIATE SOURCE:
CLONE: ACS GENE
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Best Local Similarity:
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MOLECULE TYPE: CI
ORIGINAL SOURCE:
                                               CLASSIFICATION:
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DB:
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                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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22
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                      APPLICATION NUMBER: US/09/125,642C FILING DATE: 20-Aug-1998 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/EP97/00729, FILING DATE: 17-Feb-97 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1080 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Parapox ovis
STRAIN: D1701-HD1R-Genregion
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/09255829 Patent No. 6461617 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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STREET: 100 Bayer RC
CITY: Pittsburgh
STATE: Pennsylvania
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45.93%
29.63%
10.87%
                                                      COUNTRY: U.S.A.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 ValThrAlaThrLeuMetThrAlaPhe-----ThrLeuAlaSerCysAlaSerThrPro 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 ValLysGlnThrCysGlnThr-----GlnLeuThrGlyHisGlnTyrTrpLysIleAla 61
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                                                                                  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, NW, SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                                                                             Version #1.30 (EPO)
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1581.0130002
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-A06-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2574 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: ESMOND, ROBERT W
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
                                                       NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                              CIT1.
STATE: D.
COUNTRY: USA
TP: 20005-3934
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Best Local Similarity:
Query Match:
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US-09-255-829-28
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2554 TACAGAGTCAGTAGTTGCA 2572
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 45.79%
27.10%
10.80%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEO ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kauffman
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
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US-08-658-665-71/c
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL
                                                           1319 TCAAAGCACCGGGTATCTGCATCGACGTTGACAACGAAGACCTCTTCTTCATCGCAGACA 1378
                                    96 ---ThralaalaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHis 114
                                                                                                                                       1439 ACTACATCGAAAACGACTTCCCGATCAACGAACTCATCCTCGACACCGACGTCATCA 1495
                                                                                                            115 SerLeuLysProCysMetLeuGluThrValAsnAlaPheIleValProThrThrThr 133
                                                                                                                                                                                                                                                                              APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCES: ADDRESS: ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
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29
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
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                                                                                                                                                                               RESULT 23
US-09-221-017B-311
; Sequence 311, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MODICOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98,
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Window
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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73.00
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EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304-1018
COMPUTER READABLE FORM
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Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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2260 ATAGAGTTCGTAGAGGTCGGTCTCCTTTTTGGTTTCGGGGCTCTTCGATTGCTTTAGCACC 2319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2380 AGATATCTGAGCCATATTAGCACGACGAGCCACACCCCACTACTGCACCGCCACGATTCAC 2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ::::::|||:::
2500 TACAGTAGCAGAATCAGCTACAGCTTGTACAGCA-----GCAGAATCGGCTGTTGCAGC 2553
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                                                                                                                                                                                                                                                                                                             ---SerSerAl 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 aLysileSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLe 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||
| 2440 GGGAGTAAGCAGAGAGAGAGTGCGTTTACGAGTACCATCCTTGGCCTCTTTTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                      33 aAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuTh
                                                                                                                                                                                         4 IleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 rGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLys----Al
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                                                                                                                                     US-10-048-196-2 (1-134) x US-09-221-017B-311 (1-6321)
                             Mismatches:

    Curtis, Morris & Safford, P.C.
    Fifth Avenue

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compositions and Uses 190
                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2720.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
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FILING DATE: 05-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       24 ProGlu-SerAsnProLysAsn----
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Cox, William I.
Kauffman, Elizabeth K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Sequence 71, Application US/08658665
; Patent No. 5997878
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Sequence 121, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
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Burland, Valerie
Perna, Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 eValArgHisSerLeuLysProCys 119
                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-09-085-273-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plunkett, Guy
Welch, Rod
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 6749 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                               39.45%
23.85%
10.80%
                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Madison
                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 uThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIl 111
                                                                                                                                                                                                                                                                                                      55
                                                                                                                                                                                                                           18 AlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThr 37
                                                                                                                                                                                                                                                                                                                                                                               56 ------GlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAla 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 Lys1leSerGluThrAlaCysGly-CysValAlaAspLysAlaProGluAlaValSerLe 91
                                                                                                                                                                                                                                                                                                    38 SerLeulleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHis----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,273
                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                       1754 TTGCCCTGGATGCGATACTGGCTGTG------
                                                                                                                                                                                     US-10-048-196-2 (1-134) x US-08-658-665-71 (1-6749)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Paoletti, Enzo
APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Kauffman, Elizabeth K.
TITLE OF INVENTION: RECOMBINANT POXVIRUS - C
TITLE OF INVENTION: COMPOSITIONS AND USES
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2720
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Curtis, Morris & Safford STREET: 530 Fifth Avenue CITY: New York STATE: New York COUNTRY: United States of America 21P: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/471,014
FILING DATE: 06-UUN-1995
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1616 CGCTTGCACCTCCAGGAGATCTGC 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eValArgHisSerLeuLysProCys 119
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; Sequence 71, Application US/09085273
Patent No. 626/965
; GENERAL INFORMATION:
                                                       91.8
73.00
39.45%
23.85%
10.80%
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                                                                                          Percent Similarity:
Best Local Similarity:
Ouery Match:
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                                         Alignment Scores:
 JS-08-658-665-71
                                                         Pred. No.:
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1814 TCGTCGTCGCCCTGGGCGCACCCTCGTCGTGCCGGTCCCAGGTGTGTCTCAGGTACTCAAGC 1755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 uThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIl 111
                                                                                                                                                                                                                                                                                                            55
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                                                                                                                                                                                                            18 AlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThr
                                                                                                                                                                                                                                                                                                         38 SerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHis----
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COMPUTER READALE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: No. 6365723el Sequences of E.
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
6749
26
17
45
21
                        Matches:
Conservative:
                                                                                                                                                               US-10-048-196-2 (1-134) x US-09-085-273-71 (1-6749)
                                                                    Mismatches:
Indels:
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    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
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ORIGINAL SOURCE:
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09125642C
Patent No. 6365393
GENERAL INFORMATION:
APPLICANT: BAYER AG
TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
Their Production and Their Use in Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 ThralaThrLeuMetThr---AlaPheThrLeu---AlaSerCysAlaSerThrProGlu 25
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6834 ICTCGTAACGAATCCATATTCCCTAAATACAAACATGATTCCAAGCCTTGTGCAATA 6890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 GlnThrCysGlnThrGlnLeuThrGlyHis-----GlnTyrTrpLysIleAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 MetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAla
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-048-196-2 (1-134) x US-09-453-702B-121 (1-14187)
                                                            NAME: Seay, Nicholas J.
REGISTATION WUMBER: 2736
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 121:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Bayer Corporation
STREET: 100 Bayer Road
CITY: Pittsburgh
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                        TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
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                  FILING DATE: 04-DEC-19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                               42.02%
29.41%
10.80%
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                                                                                                                                                                                                                           LENGTH: 14187
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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832 CTCCGGTAGCGCGGATGC-------GCCGGCGCGCGCGCCACACAAAGGCCACGGC 785
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US-09-125-642C-12/C
; Sequence 12, Application US/09125642C
; Sequence 10. 6365393
; GENERAL INCRMATION:
APPLICANT: BAYER AC
TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, a
TITLE OF INVENTION: Production and Their Use in Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SerLysAl
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                              Fragment I (Version 1) NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrPro----
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40
21
46
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 aGlnLysIleValArgHisSerLeuLys---ProCysMetLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                      FILING DATE: 20-Aug-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/00729,
FILING DATE: 17-Feb-97
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERASTICS:
LENGTH: 5515 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-048-196-2 (1-134) x US-09-125-642C-8 (1-5515)
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                                     APPLICATION NUMBER: US/09/125,642C
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ADDRESSEE: Bayer Corporation
STREET: 100 Bayer Road
CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Parapox ovis
STRAIN: D1701- HIND III
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                 CURRENT APPLICATION DATA:
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72.50
45.198
29.638
10.728
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954 TCCTTGCTGACCAGCACGACCAGCGCGCTCACGGCCGGTGTGCCGAGCATGCTGCGGGAA 895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 570 GTTGCGTTTGACGACGTGTCGAGATCGGTGTGCGTCCGGCGGCGCTGACACGACGGGGG 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 aLysileSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSer-- 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 aMetLysLeuSerSerGlu-----SerLysAl 71
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                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLys---
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Parapox ovis
STRAIN: D 1701, HindIII-Fragment I,
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                APPLICATION NUMBER: PCT/EP97/00729,
FILING DATE: 17-Feb-97
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,642C
FILING DATE: 20-Aug-1998
PRIOR APPLICATION DATA:
                                 ZIP: 15205-9741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 5519 base pairs
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09144085 Patent No. 6280999 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid_STRANDEDNESS: double
STATE: Pennsylvania
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72.50
45.19%
29.63%
10.72%
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
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29026 ATCGCCTCCACACCCAGGGCTTCGCCCACGCCCTCGCCCTCAGGCGCAGGAGCACC 28967
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| 28810 GCGGCA-----TCTGTAACGCGCAGCGAGGCGGCTGCCTGTGCCGAGTCTCTGCCTCT 28757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 TyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThr 76
                APPLICANT: Ashley, Gary
APPLICANT: Julien, Bryan
APPLICANT: Ziermann, Rainer
TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
TITLE OF INVENTION: THERREDR
FILE REFERENCE: 30062-20020.20
CURRENT APPLICATION NUMBER: US/09/144,085
CURRENT FILING DAPE: 1998-08-31
EARLIER APPLICATION NUMBER: 09/010,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GlnLysIleValArgHisSerLeuLysProCysMetLeu----
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Conservative:
Mismatches:
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APPLICANT: Shenbagamurthi, Ponniah
APPLICANT: Culler, Michael D.
APPLICANT: Setcavage, Diane R.
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Patent No. 5472865
GENERAL INFORMATION:
APPLICANT: Harris, Crafford A.
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Siekierka, John J.
                                                                                                                                                                                                                                                                                                                ORGANISM: Sorangium cellulosum US-09-144-085-3
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72.00
36.96%
26.81%
10.65%
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SOFTWARE: PatentIn Ver. 2.0
Betlach, Mary C.
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Best Local Similarity:
                                                                                                                                                                                                                                                                          LENGTH: 33529
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US-08-171-382-1/c
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                                                                                                                                                                                                                                                                                                 TYPE: DNA
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30
118
41
42
            STREET: Spring House Corporate Cntr, P.O. Box 457 CITY: Spring House STATE: Pennsylvania
                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,382
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                   TELEPHONE: 514
ATTORNEY/AGENT INFORMATION:
NAME: BAK, MATY E
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: 31,215
REFERENCE/COCKET NUMBER: IR143USA
TELEPHONE: 215-540-9206
TELEPHONE: 215-540-9206
TELEPHONE: 215-540-9218
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: PATENTIN Release #1
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Howson and Howson
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.7
71.50
43.24%
27.03%
10.58%
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LOCATION: 205..2286
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Best Local Similarity:
Query Match:
                                                                  COUNTRY: USA
                                                                                                                                                                                                                        FILING DATE:
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US-08-309-420-1/c
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TITLE OF INVENTION: Method for the Diagnosis of Depression TITLE OF INVENTION: Based on Monitoring Blood Levels of Arginine Vasopressin TITLE OF INVENTION: and/or Thymopoietin
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1838 GAAATAAACCCTAGGATTTCATCATCTATTGGAACTGATAATATCTGTGTTGCCTCC 1779
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                                                                                                                                                                                                                                                                                       SOFTWARE: PATENTEN PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/309,420 FILING DATE:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                            ADDRESSEE: Howson and Howson
STREET: 321 No. 5591588ristown Road, Box
CITY: Spring House
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                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAK, MARY E.
RECISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR14f
TELEPHONE: (215) 540-9207
TELEPHONE: (215) 540-9207
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2490 base pairs
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71.50
43.24%
27.03%
10.58%
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STRANDEDNESS: double
                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 205..2286
                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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Best Local Similarity:
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US-08-309-420-1
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89 ValSerLeuThrGluLeuThrThrAlaAla-IleAsnProAsnAlaArgThrGluValAl 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version#1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11856
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
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Matches:
                                                                                                              1553 TTCTGAAATGCCACAAAGGAACCTGAATCCC 1523
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                                                                                    . 108 aGlnLysIleValArgHisSerLeuLysPro 118
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STREET: 321 Norristown Road, Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,419
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BAK, MATY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR145
TELECOMMUNICATION INPORMATION:
TELEPHONE: (215) 540-9206
TELEPHONE: (215) 540-9206
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2490 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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1838 GAAATAACCCTAGGATTCATCATCTTTTGGAACTGATAATATCTGTGTTGCCTCC 1779
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1718 TCTTCTTCAATTACT-----TTTAAAATAGATTCATGGAAGGAAAAGATAGT 1671
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                                                                                                                       GENERAL INFORMATION:
APPLICANT: Goldstein, Gideon
APPLICANT: Culler, Michael
TITLE OF INVENTION: Method of Measuring Thymopoietin
TITLE OF INVENTION: Proteins in Plasma and Serum
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: 321 No. 5593842ristown Road, Box 457
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,419
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Matches:
Conservative:
Mismatches:
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1553 TTCTGAAATGCCACAAAGGAACCTGAATCCC 1523
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Bak, Mary E.
REGISTATION UNUBER: 13,215
REFERENCE/DOCKET UNUBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-506
TELEFAX: (215) 540-5018
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                           US-08-309-419-1/c
; Sequence 1, Application US/08309419
; Patent No. 5593842
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27.038
10.58%
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EDNESS: double
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205..2286
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                                            RESULT 32
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1838 GAAATAAACCCTAGGATTTCATCATCTATTGGAACTGATAATATCTGTGTTGCCTCC 1779
1613 GTGAGTGAATGAGAGACAGTTTTGGCAAAAGAAGACATCAGTTCGGATCCAGGTATG 1554
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                                                                                                                                                                                                                  FOCT-US95-11856-1/C
Sequence 1, Application PC/TUS9511856
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Method of Measuring
TITLE OF INVENTION: Thymopoietin Proteins in Plasma and Serum
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
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Db 1838 GAAATAAACCCTAGGATTTCATCATCTTTTGGAACTGATAATATCTGTTGCCTCC 177	Oy 41	Qý 49 GlnThrGlnLeuThrGlyHisGlnTyrTrpLysIlealaalaalaactysLeuSerSerGlu 68 ::: ::: ::: :::	Oy 69 SerLysalaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAla 88	Oy 89 ValSerLeuThrGluLeuThrThrAlaala-IleAsnProAsnAlaargThrGluValal 108	Qy 108 aclnLysileValArgHisSerLeuLysPro 118 :::::::::::::::::::::::::::::::::::	RESULT 35 US-09-010-809-14/c ; Sequence 14, Application US/09010809B	; Patent No. 6090601 ; GENERAL INFORMATION: ; APPLICANT: Gustafsson, Claes	TITLE OF INVENTION: Therefor;	; FILE REPRENCE: 30062-20020.00 ; CURRENT APPLICATION NUMBER: US/09/010,809B ; CURRENT FILING DATE: 1998-01-22	; NUMBER OF SEQ 1D NOS: 23 ; SOFWHARE: Patentin Ver. 2.0 . SFO ID NO 14	TYPE DNA TYP		US-09-010-809-14 Alignment Scores:	8.2 Length: 70.00 Matches: 35.34% Conservative:	Mismatches: Indels: Gaps:	(1-794)	Qy 17 LeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThr 36	37 ThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGln	Db 717 ACCAGCGAGTCCACGTTGGAGCCGCCTCCACGAGGTCACGAGG 673	Qy 57 TyrTrpLys	Oy 66 SerSerGluSerLysAlaLys72	Db 615 TCGGCCGTCGCCGGCGAGATGCAGGGCACCGACGCTCACCACCGGCTGGCCGGCGGCA 556
::: :: :: Db 1718 TCTTCTTCAATTACTTTTAAATAGATTCATGAAAGGGAAAAGATAGT 1671	Oy 69 SerLysalaLysIleSerGluThrAlaCysGlyCysValalaaspLysAlaProGluala 88 	Oy 89 ValSerLeuThrGluLeuThrThrAlaAla-IleAsnProAsnAlaArgThrĠluValAl 108 	Oy 108 aGinLysileValArgHisSerLeuLysPro 118 Db 1553 TTCTGAAATGCCACAAAGGAACCTGAATCCC 1523	RESULT 34 PCT-US95-11878-1/c ; Sequence 1, Application PC/TUS9511878 . GENERAL INFORMATION	APPLICANT: Immunoblology Research, Institute Inc.; TITLE OF INVENTION: Method for the Diagnosis of; TITLE OF INVENTION: Depression Based on Monitoring Blood Levels of; TITLE OF INVENTION: Arginine Vasopressin and/or Thymopoletin	; NUMBER OF SEQUENCES: 7 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Howson and Howson	SIREET: 3.1 NOTIBLOWN ROBD, BOX 45/ CITY: Spring House; STATE: PA COUNTRY: USA	PADABI	patible -DOS/MS-DOS	CURRENT APPLICATION DATA: CURRENT APPLICATION NUMBER: PCT/11895/11878		; APPLICATION NUMBER: US 08/309,420 ; FILING DATE: 20-SEP-1994 ; ATTORNEY/AGENT INFORMATION:	; NAME: BBK, MBYY E. ; REGISTRATION NUMBER: 31,215 ; REFERRENCE/DOCKET NUMBER: IR146PCT	; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (215) 540-9206 ; TELEFAX: (215) 540-5818	; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 2490 base pairs	; TYPE: nucleic acid ; STRANDEDNESS: double ; TODA COT	. . .	; LOCATION: 2052286 PCT-US95-11878-1	Length:	11.50 Matches: 11arity: 43.24% Conservative: Similarity: 27.03% Mismatches:	Indels: Gaps:	US-10-048-196-2 (1-134) x PCT-US95-11878-1 (1-2490)

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83.AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla---IleAsnPro 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 ThralaThrLeuMetThralaPheThrLeuAlaSerCysAlaSerThrProGluSerAsn 27
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                                                                             495 CTCACCCGGANCTCGCTCGCCCCCGTGCCACGCCACCCANTCCGAA 448
                                                   LeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGlu 106
                                                                                                                                                                       APPLICANT: KUranda, Michael J.
TITLE OF INVENTION: IMMOBILIZATION AND PURIFICATION OF: FUSION PROTEINS USING CHITIN-BINDING ABILITY
                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/303,827
FILING DATE: 30-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application.US/08209747
Patent No. 5733771
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70.00
37.95%
22.29%
10.36%
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APPLICANT: Lewis,
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                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                            ; Patent No. 5258502
                                                                                                                                                                                                                                                                                                                      LENGTH: 2214
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Pred. No.:
                                                                                                                                                                                                                                                                                                      ;SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
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Lewis, Randolph V.

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                              CDNAS Encoding Minor Ampullate Spider Silk Proteins
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OTHER INFORMATION: /product= "N. clavipes minor
OTHER INFORMATION: ampullate silk protein"
                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
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APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAS Encoding Minor Ampu
TITLE OF INVENTION: Silk Proteins
TITLE OF INVENTION: Silk Proteins
CORRESPONDENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: BIrch, Stewart, Kolasch & Birch
CITY: Falls Church
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Indels:
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                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/209,747
FILING DATE: 14-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGIGSRATION NUMBER: 28,977
REFERENCE/CDCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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19.27%
10.28%
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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Best Local Similarity:
Query Match:
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ORGANISM: Nep
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NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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Best Local Similarity:
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                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: cDNAS Encoding Minor Ampullate Spider
TITLE OF INVENTION: 511k Proteins.
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2793
21
27
26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
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STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Nephila clavipes
TISSUE TYPE: minor ampullate gland
                                                              1886 CTCCAGCAGCTGCCGCAGCAGCTC 1860
                                 108 AlaGlnLysIleValArgHisSerLeu 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/458,298
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
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APPLICATION NUMBER: US 08/209,747
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 Sequence 1, Application US/08458298
Patent No. 5756677
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS
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TELECOMMUNICATION INFORMATION
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2793 base pairs
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69.50
44.048
19.278
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STRANDEDNESS: double
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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Best Local Similarity:
Query Match:
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ORGANISM: Nep
                                                                                                               US-08-458-298-1/C
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                                              2110 AGCTCCTGCAGCGGCTCCAGCACCAGCACCTAACGTAACCACCAGCGCCTCCGGATCC 2051
                                                                                                                                  88 AlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluVal 107
                                                                                                                                                                                                68 GluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGlu 87
28 ProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThr 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CROUZET, Joel
APPLICANT: FAMECHON, Alain
APPLICANT: FERRERO, Lucia
APPLICANT: FERRERO, Lucia
TITLE OF INVENTION: No. 6001631e1 Topoisomerase IV, Corresponding
TITLE OF INVENTION: Nucleotide Sequences and Uses Thereof
                                                                                                48 CysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                108 AlaGlnLysIleValArgHisSerLeu 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,265
FILING DATE: 24-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08776265 Patent No. 6001631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
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TELECOMMUNICATION INFORMATION
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                          1285 ACGTGTTTCATTTTTGTGACTTTTTTACTTAACATAAATCAGCTTCCACTAAGACGCCC 1344
                                                                                                                                                                                                                                                                                                                                                                                1345 TCCAAGTCGTTTTGAACCTGCTCTGGCGTTTAAGGTTCGCTATAATGGTAATGCACCATT 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1465 TTAATAGGFGFGFTAGCCCCGTCCGCA---ACCAFGACFGAAATTTTAACFFCTATCAFT 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 AsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCys 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 CysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIle 99
                                                                                                                                                                                                                                                                                                                                                                                                                                ------MetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly 79
                                            13 ThralaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSer 32
                                                                                                                                                                                                                                       ThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAla------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Cloning and Expression of Microbial TITLE OF INVENTION: Phytase NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSEE: Morrison & Foerster STREET: 545 Middlefield Road, Suite 200 CTTY: Mendo Park STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1525 ------ATTAGCACATTAATACTGACTACGACT 1554
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                                                                                                                                         33 AlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGln
US-10-048-196-2 (1-134) x US-08-776-265-2 (1-4565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robert F.M. Van Gorcom
Willem Van Hartingsveldt
Petrus A. Van Paridon
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APPLICATION NUMBER: US/08/151,574
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REJETRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Rudolf G.M. Luttin
Gerardus Selten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 ThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGln 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThr 36
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                                                                                                                                                                                                                                                        ORGANISM: Aspergillus ficuum (Aspergillus niger)
STRAIN: NRRL 3135
INMEDIATE SOURCE:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Phytase"
/evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
24615-20026.00
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LOCATION: join(210..253, 356..1715)
OTHER INFORMATION: /codon_start= 210
OTHER INFORMATION: /product="Phytase"
                                                                                                                                                                                                                                                                                                                   LIBRARY: lambda AF
CLONE: pAF2-3, pAF2-6, pAF2-7
            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 6756 base pairs
TYPE: nucleic acid
STRANJENNESS:
                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
REFERENCE/DOCKET NUMBER:
                                                                                                                                         double
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210..253
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Best Local Similarity:
Query Match:
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ORIGINAL SOURCE
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NAME/KEY:
LOCATION:
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6058 ACTTGGATACACCCGGAATCGAACGCAGTACTCCGTACGGCGAAAGTTTTCCTTTTGAAT 5999 q

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Search completed: May 5, 2003, 23:20:00 Job time : 66 secs

Scoring table:

Total number

Searched:

Perfect score:

Sequence:

OM protein

Run on:

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TITLE OF INVENTION: No. US20030023075Alel Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESSE: Quarles & Brady STREET: 1 South Pinckney Street
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Sequence 46,
Sequence 46,
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Sequence
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             US-09-738-626-2345
US-09-138-626-524
US-10-152-661-524
US-10-152-661-587
US-09-866-050A-587
US-09-864-761-19149
US-09-804-761-19149
US-09-804-761-152
                                                                                                                                      APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 132, Application US/10114170
Publication No. US200330233075A1
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick
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Perna, Nicole T.
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Welch, Rod
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ZIP: 53701-2113
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    RESULT 1
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-MODEL-frame+p2n.model-USDV=x1h
-MODEL-frame+p2n.model-USDV=x1h
-MODEL-frame+p2n.model-USI0048196/runat_28042003_151442_5681/app_query.fasta_1.327
-C0=/Cgn2_1/USPTO_spool/USI0048196/runat_28042003_151442_5681/app_query.fasta_1.327
-DB=Published_Applications_NA -GPMT-fastap -SUFFIX*rnpb -MINNATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=0
-THR_MIN=0 -ALIGN=40 -MODE-LCAL -OUTFWT=pto -NORM=ext -HEAPBIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=USI0048196_GCGN_1_1.84_Grunat_28042003_151442_5681
-NCPU-6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NGS_SCORES=0 -WAIT -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -PGLOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4588, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 132, App
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                                                                                                                              (without alignments)
1759.303 Million cell updates/sec
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                                                                                                                                                                                           676
1 MMKILYVTATLMTAFTLASC.....SLKPCMLETVNAFIVPTTTR 134
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
//cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
//cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                                                                                                             ; Search time 90 Seconds
                   GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                - nucleic search, using frame_plus_p2n model
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US-09-815-242-8609
US-08-781-986A-447
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                                                                                                                                                                                                                                                                                                                                                                  of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   746064 seqs, 590810554 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_NA:*
                                                                                                                                                                                                                                                    Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match Length DB
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66:
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113:
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Database :

Score

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1249 ATGCCTGCCGCTTTAGCATTAACCAGGGAATGACGTCGCATACTAACTCTGGCGTGGCG 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1462 TGGGTGACAAGGTAAGTACGGGTCAGTTTTTGGTAATCTCTGGAGTGACATCAGAAACA 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1189 GTAATCAGTTTGACAAGCGCTTTACGCCACTCTTTATCTTCATGTATTGCCAGCAAAGTA 1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 LysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLys 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 TyrValThrAlaThrLeuMetThrAlaPhe---ThrLeuAlaSerCysAlaSerThrPro 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 GluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaVal
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                         NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEPHONE: (608) 251-5166
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-048-196-2 (1-134) x US-10-114-170-132 (1-3823)
                                                                                                                                                                                                                                                                                                                              ;
SEQUENCE DESCRIPTION: SEQ 1D NO: 132:
US-10-114-170-132
               APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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Patent No. US20020061569A1
GRERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
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Zyskind, Judith W.
Wall, Daniel
PRIOR APPLICATION DATA:
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36.91%
22.15%
12.65%
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                              LENGTH: 3823
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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APPLICANT:
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539 ATGCCACCAGTACATACGTAACC -- - ACTTTTTATCTGCAAATAACGCTTTATTCTCT 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 TCTTCTTCTAAATCTAAAGCAACAATCTCTTTTCGAGGACGTACATGCATTTTCTTAAAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 AsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGln 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 Ala---ProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
                                   APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
FILE REPRENCE: ELTRA.OILA
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PAPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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134
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Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8609, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus
                         amamoto, Robert T.
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Zyskind, Judith W.
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
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45.30%
29.06%
12.43%
Grant
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Best Local Similarity:
Query Match:
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FILING DATE: ATTORNEY/AGENT INFORMATION:
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29.06%
12.43%
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                        Maryland
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Best Local Similarity:
Query Match:
 GENERAL INFORMATION:
                                                                                                                                                                       20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-781-986A-447
                                                                                                                                   STATE: Ma
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185 TTAATCCAGTCAGGCAAATCTCTAAAGCGCGTGATATTTGGACGAATTGCACCTCGGAAA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 TCTTCTTCTAAATCTAAAGCAACAATCTCTTTTCGAGGACGTACATGCATTTTCTTAAAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542 ATGCCACCAGTACATACGTAACC---ACTTTTTATCTGCAAATAACGCTTTATTCTCT 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 LeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKATYOUS

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR PELICATION NUMBER: 60/19,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR PELICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,77

PRIOR FILING DATE: 2000-05-23

PRIOR PRIOR DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR PRIOR APPLICATION NUMBER: 60/253,938

PRIOR PRIOR DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22
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34
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-048-196-2 (1-134) x US-09-815-242-8609 (1-957)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-781-986A-447/c
; Sequence 447, Application US/08781986A
; Publication No. US20030054436A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuAlaSerCysAlaSerThr---
                                                   Yamamoto, Robert T.
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45.30%
29.06%
12.43%
Daniel
                              Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-815-242-8609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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APPLICANT: Charles Kunsch
THILE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 TGACCTAAATCAAATTCATAATCATTACGTGCATCAATAATGACTGTGTCATCATCTTCA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 AGAGCTTTTCTAAATTCTACAGGTGATAAATAFTGGCCAGTTGTGTGTCTTGGATCGACG 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 AsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGln 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 LeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys
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                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-048-196-2 (1-134) x US-08-781-986A-447 (1-1799)
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Mismatches:
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Matches:
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                                                                                                             Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Benson, Bob
REGISTRATION UNBER: 30,446
REFERENCE/DOCKET NUMBER: PB24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 447:
SEQUENCE CHARACTERISTICS:
                                                                                                       ADDRESSEE: Human Genome Scie
STREET: 9410 Key West Avenue
CITY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2065 GAGAATTGAATGATTTTGTTTCAACTGCCAAAGGTGTGTTGCAGTCACTCATTGAAAAAC 2124
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                                                                                                                          APPLICANT: RESOLICY, RICHARD 1.
APPLICANT: Resolick, Richard 3.
APPLICANT: Resolick, Ramalakar
APPLICANT: Glukotta, Kamalakar
APPLICANT: Grabham, James R.
APPLICANT: Greetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR PPLICATION OFFEE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 SHisAlaValLys-----GlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 lyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1996 AATGTGTTGTAATTGGTCTGCAGTCTACAGGAGAAGCTAGA-----
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Mismatches:
Indels:
Gaps:
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Matches:
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Sequence 489, Application US/09822849A Patent No. US20020045170A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AlaSerThrProGluSer------
                                                                                            Fechtel, Kim
Agostino, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.455
79.50
41.56%
25.32%
11.76%
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 489
LENGTH: 2456
                                                       APPLICANT: Wong, Gordon G.
                                                                        Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-822-849A-489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                   GENERAL INFORMATION:
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                                                                          APPLICANT
                                                                                          APPLICANT
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57 TCCAGCAGTGATTCCTTTCGGAGTCAAGCACCTCTTCTTCCACCTCTTTCGGCTGCG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 CAGGGT-----TCTGAGAACGCTCCTGAGCTG-----TTTGAGACCATGACTCAGGCA 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 LysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIle 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGlu-----ThrAla 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 CysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAla 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 AlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleVal 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 AAGGTGGAGTCGGGTGCTGAGTTCCAGGTTGTTGGTTCTGTGCTT 321
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JF 99/317484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Corynebacterium glutamicum US-09-738-626-2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 524, Application US/10152661
Publication No. US20030022835A1
GENERAL INFORMATION:
                     MIZOGUCHI, HIROSHI
                                                                                                                              TATEISHI, MACKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene
SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
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47.83%
23.48%
11.61%
                                                                  HAYASHI, MIKIRO
                                                                                     OCHIAI, KEIKO
YOKOI, HARUHIKO
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                                          ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER ... SOFTWARE: Paten SEQ ID NO 2345
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 AGGCGGTGAATATCCGGGGCAAGCTGGTGTCGCTGGAGAAGTACCGCGGGCTCGGTTTCCC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 ---TrpLysleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 LeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyr--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 rccrgrcgcccccccccccaccarcccaccaaccrrcr-----accaccrrca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSer---LeuThrGluLeuThr
              ITLE OF INVENTION: Compositions Isolated From Skin Cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             980
33
20
53
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                        FILE KEFEKENCE: 1100.10110.10110.
CURRENT PELLING DATE: 2002-05-20
PRIOR FILING DATE: 2002-05-20
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 1900-07-25
PRIOR FILING DATE: 1900-07-24
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-04-29
PRIOR PILING DATE: 1999-04-29
PRIOR PILING DATE: 1999-04-29
PRIOR PILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 725
SOFTWARE: PASESEQ for Windows Version 4.0
SSOFTWARE: 980
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Kumble, Krishanand D.
                                                 ILE REFERENCE: 11000.1011c5
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27.058
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Query Match:
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US-10-152-661-524
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155 TGGTGGTGAATGTAGCTAGCGAATGTGGCTTCACAGACCAGAACT-----ACGGAGCCT
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PPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
                                         APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 09/866,050
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Sleeman, Matthew
Onrust, Rene
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Sleeman, Matthew
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                            Onrust, Rene
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Query Match:
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US-09-866-050A-524
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LENGTH: 980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 MetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSer
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: On Unst, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
APPLICANT: Kumble, Krishanand D.
APPLICANT: Murison, James G.
APPLICANT: Matthewath Ma
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                     PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/206,650
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR PLING DATE: 1998-11-09
PRIOR PLING DATE: 1998-11-09
PRIOR PLING DATE: 1998-10-05
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 725
SEQ ID NOS: 725
SEQ ID NO 587
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APPLICATION NUMBER: 60/221,232
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/09/664,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US/09/664,761

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-08-03

PRIOR PELING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 60/235,356

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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Percent Similarity:
Best Local Similarity:
Query Match:
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LENGTH: 2324
TYPE: DNA
ORGANISM: Mouse
                                                                                       US-09-866-050A-587
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Salama, Sofie
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SerLysAlaLysIleSerGluThrAla 77
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N: EXPRESSED IN PLACENTA, SIGNAL = 1.7
N: EXPRESSED IN BRAIN, SIGNAL = 2.4
N: EXPRESSED IN HETAL LIVER, SIGNAL = 1.8
N: EXPRESSED IN HETAL, SIGNAL = 2.1
N: EXPRESSED IN HETA, SIGNAL = 1.5
N: EXPRESSED IN HELA, SIGNAL = 1.5
N: EXPRESSED IN HELA, SIGNAL = 1.5
N: EXPRESSED IN BOLLOO, SIGNAL = 2.7
N: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
N: SWISSPROT HIT: P04929, EVALUE 2.00e-06
                                                 PRIOR FILING DATE: 2001-01-30
PRIOR PILICATION NUMBER: PCT/USOLI/00003
PRIOR PELICATION NUMBER: PCT/USOLI/00003
PRIOR APPLICATION NUMBER: PCT/USOL/00661
PRIOR APPLICATION NUMBER: PCT/USOL/00661
PRIOR APPLICATION NUMBER: PCT/USOL/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PRIOR DATE: 2001-01-29
NUMBER: OF SEQ ID NOS: 49117
SEQ ID NO 19149
LENGTH: 1161
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Conservative:
Mismatches:
Indels:
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                 R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/US01/00663
R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/US01/00662
R APPLICATION NUMBER: PCT/US01/00661
R APPLICATION NUMBER: PCT/US01/00661
R APPLICATION NUMBER: PCT/US01/00670
R FILING DATE: 2001-01-30
R FILING DATE: 2001-01-30
R FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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US-09-864-761-19149
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFRENCE: 10972.147
CURRENT PAPLICATION NUMBER: 05/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1099-10-20
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTHARE: PATCHIN VERSION 3.0
SEPTARE: PATCHIN VERSION 3.0
LENGTH: 1818
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Mismatches:
Indels:
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Matches:
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No. US20020128250Alman, Thea
Sequence 427, Application US/09801368 Patent No. US20020128250A1
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                                                                       APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
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                                         APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475c10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FESLSEQ for Windows Version 3.0
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Conservative:
Mismatches:
Indels:
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Patent No. US/0020110563A1
GENERAL INFORMATION:
APPLICAMT: Reed, Steven G.
APPLICAMT: Henderson, Robert A.
APPLICAMT: Lodes, Michael J.
Application US/09854133
5. US20020183499A1
                                                                                                                                                                                                                                                                                                                                                       1.03
76.50
40.91%
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                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapien US-09-854-133-152
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Best Local Similarity:
Query Match:
Sequence 152, Applic
Publication No. US20
GENERAL INFORMATION:
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US-09-738-973-152
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LENGTH: 2179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 sile-AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 lyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----Ser-LeuIleLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 sHisAlaValLys-----GlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09819505
Patent No. US/0201412417A1
GENERAL INFORMATION:
APPLICANT: Paigen, Beverly
Beier, David R.
TILE OF INVENTION: of Use Therefor
                                                                                                                                          APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEO ID NOS: 587
SOFTWARE: FASLSEQ for Windows Version 3.0
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39
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                    Algate, Paul A.
Secrist, Heather
Indirias, Carol Yoseph
Benson, Darin R.
Elliot, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AlaSerThrProGluSer----
Fling, Steven P. Mohamath, Raodoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.03
76.50
40.91%
25.32%
11.32%
                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapien
US-09-738-973-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1707 -----
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                 SOFTWARE: FR
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                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                              APPLICANT
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No.:
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APPLICANT: Collmer, Alan
APPLICANT: Alfano, James R.
APPLICANT: Charkowski, Amy O.
APPLICANT: Charkowski, Amy O.
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         632 ---GGCCTGAGGATGTCAGCTGGCAGCCGTGCTTCCAGCTCCGTAGAAGATC 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 ValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 TCCCTAAAGGAGTCTTCACCAAAGAGCTCCCGTCTGGCAAAAAATACCTCCGTTATACAC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        578 CCCAGCCTTAAGTCTTTGCGGAAATTGGGGCTGCATCTGCACATCCAGTACTGG----- 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLys 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 HisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHis---GlnTyrTrpLysIle 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaalaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCys, 80
                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/09/819,505
FILING DATE: 28 Mar-2001
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: FETTEll, Kevin M.
REGISTRATION NUMBER: 35.505
REFERENCE/DOCKET NUMBER: JL-2001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0528
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 3;
                                                                                                                        COUNTRY: USA
2IP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09825414 Patent No. US20020083489A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1193 base pairs
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Farrell & P
STREET: P. O. Box 999
CITY: YORK HARBOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.782
74.50
50.00%
29.27%
11.02%
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 rGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleVa 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 lArgHisSerLeuLysProCysMetLeuGluThrValAsnAlaPheIleValProThrTh 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 GlnTyrTrpLysIleAlaAlaMetLysLeuSer-----SerGluSerLysAlaLys 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 IleSer-GluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10071338
Publication No. US20030022321A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030022321A1e1 compounds
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30365
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22
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                        n at any position is undefined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
FILE REFERENCE: 19603/3243
CURRENT APPLICATION NUMBER: US/09/825,414
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/124,160
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-08-11
PRIOR PRICATION NUMBER: 60/249,548
PRIOR FILING DATE: 2000-11
PRIOR FILING DATE: 2000-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SmithKline Beecham
                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.50
42.28%
24.39%
11.02%
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COUNTRY: UK
                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3147 GGCGCGC 3141
                                                                                                                                                                                                                                                                                                                                                               LOCATION: (29734)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 rThrArg 134
                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
                                                                                                                                                                                                                                                            LENGTH: 30365
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                                                                                                                                                                                                                                        SEQ ID NO 1
                                                                                                                                                                                                                                                                             TYPE: DNA
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No
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; OTHER INFORMATION:
US-09-972-186A-1
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Best Local Similarity:
Ouery Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TGCTCTGTCCGTCGTTCTTCGGCCGGGACCACACCGGGT 4824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 ValArgHisSerLeuLysProCysMetLeuGluThrValAsnAlaPhelleValProThr 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 SerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGln 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ThrProGluSerAsnProLysAsnSer 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 LeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 ThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 LysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4907 GTTACGCCATGTACGCCACGCCGAACGCCGACGGACGTGG-----
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29
12
48
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                                                                      OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/071,338
FILING DATE: 08-Feb-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-048-196-2 (1-134) x US-10-071-338-1 (1-7193)
                                                                                                                                                                                                                                                                NAME: Valentine, Jill B
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: P31731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11near
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                           APPLICATION NUMBER: <Unknown>
                                                        COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 18
US-09-972-186A-1
Sequence 1, Application US/09972186A
Patent No. US20020137153A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 7193 base pairs
                                                                                                                                                                                                                             FILING DATE: <Unknown>
ZIP: TW8 9EP
TTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ThrLeuAlaSerCysAlaSer----
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 0181-9756294
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                            TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.61%
23.77%
10.87%
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Best Local Similarity:
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APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: COX, ANTHON,
APPLICANT: COX, ANTHON,
APPLICANT: OAIS, S. CHRISTOPHER
TITLE OF INVENTION: ENANTIOSELECTIVE PRODUCTION OF AMINO CARBOXYLIC ACIDS
TITLE REPERENCE: 02-1081100S
CURRENT APPLICATION NUMBER: 05/09/972,186A
CURRENT FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 GACGCCGCAAGCTCAAGCTCGACCCATCGGTTCGGTATACGGAAAAGGGT 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 ATGGCGGCAGCTTGTACATGACCCAGCTCATCGACGCCGATGGGCAACTGGTCGCCC 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 -------CysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 AGCATTTCCAGACGCTCACCAAGTACGCAATGTACTCGATGCACGAGCAGGTGCACGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description of Artificial Sequence: Synthetic nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 GluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluVal 107
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Indels:
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; Patent No. US20020061569A1
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ORGANISM: Artificial Sequence
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Carr, Grant J.
Yamamoto, Robert T
Xu, H. Howard
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Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Haselbeck, Robert
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25.22%
10.80%
AMER, SANDRA W.
HUISMAN, GJALT
                                             MILLIS, JIM
SHELDON, ROGER
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SEQ ID NO 7375
LENGTH: 10429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 ACCTCTTGCGGCAGCTTATCC----AGACCCGGCGGCGCGTCACGCGAGTATCCATC--- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 ThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHis 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ThrLeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeu 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 GlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGlu 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 ThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThr
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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT PILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SO ID NOS: 10231
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 ThralaalaIleAsnProAsnAlaArgThrGluValAlaGlnLys 110
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Matches:
Conservative:
Mismatches:
Indels:
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                                THILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-216
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASLESEQ for Windows Version 4.0
SED ID NO 9978
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73.00
45.26%
26.32%
10.80%
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ORGANISM: Salmonella typhi
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Best Local Similarity:
Query Match:
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US-09-815-242-9978
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Welch, Rod TITLE OF INVENTION: No. US20030023075Alel Sequences of E. coli 0157 CORRESPONDENCE ADDRESS:
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8353 CCCACTAGACATGTCACTGTCAGAGAAATTAAGAAAAGGTGTCTCTAACACCCAGCTATCA 8294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LysHisAlaVal-------53
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                                                                                                                                                                                                                                                                                                                                  4 IleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThr
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ZIP: 53701-2113
COMPUTER: ENDABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PATE: PC-DOS/MS-DOS
SOFTWARE: WORD PATE:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION AUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                 US-10-048-196-2 (1-134) x US-09-764-891-7375 (1-10429)
                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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Publication No. US20030023075A1
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick I Burland, Valerie Perna, Nicole T.
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STREET: 1 South Pinckney St
CITY: Madison
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                                                                                                                 39
73.00
39.84%
26.02%
10.80%
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-7375
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Percent Similarity:
Best Local Similarity:
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                                                                                             Alignment Scores:
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DB:
                                                                                                                      Pred. No.:
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374 GCGGCAAGAACTTCACAAACTACGGCTCCGACCGTCTCCGGAGCAGCAGACTCATTCAAAA 433
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: DECKARYOTES

CURRENT APPLICATION NUMBER: 08/09/815,242

CURRENT PELING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-23

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-24

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PRIOR DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-12-27

PRIOR FILING DATE: 2000-12-27

PRIOR FILING DATE: 2001-02-16
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Mismatches:
Indels:
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379 SEQ ID NO 1071 LENGTH: 1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4580, Application US/09815242 Patent No. US20020061569A1
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                   ORGANISM: Arabidopsis thaliana US-09-938-842A-1071
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Zyskind, Judith W.
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72.00
46.59%
27.27%
10.65%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 ThralaThrLeuMetThr---AlaPheThrLeu---AlaSerCysAlaSerThrProGlu 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 GlnThrCysGlnThrGlnLeuThrGlyHis-----GlnTyrTrpLysIleAlaALa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 MetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAla
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                           RAME: Seay, Nicholas J.
REGISTATION UNBER: 27386
REFERENCE/DOCKET MUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 121:
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DIA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 121: US-10-114-170-121
                        FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
  APPLICATION NUMBER: 09/453,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1071, Application US/09938842A Patent No. US20020160378A1 .
                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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29.41%
10.80%
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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Best Local Similarity:
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DB:
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Percent Similarity:
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LENGTH: 454
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                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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Mismatches:
Indels:
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Matches:
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CURRENT APPLICATION NUMBER: US/99/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8291, Application US/09815242 Patent No. US20020061569A1
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR FILING DATE: 2000-12-22
                                   ; TYPE: DNA; ORGANISM: Staphylococcus aureus
US-09-815-242-4580
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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; SEQ ID NO 4580
; LENGTH: 7104
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6193 CCTGCAACAGAAGCAGATAATGCAACGCCAGCAGAAAGCGCAACAAATAACAATAGTACA 6252
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APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3:0
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Matches:
Conservative:
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Matches:
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Gaps:
    FastSEQ for Windows Version 4.0
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; Sequence 28770, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
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US-09-918-995-28770
SOFTWARE: FastSEQ for Windows Ver
SEQ ID NO 8291
TOTSH: 7107
TYPE: DNA
ORGANISM: Staphylococcus aureus
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LOCATION: (1)...(454)
                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (1)...(7107)
US-09-815-242-8291
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                                                                                                          193 TGGGACCCAAGATCACCTATCAGGTCCCTGAAGACTTCATCTCCCGAGAGCTGTTTGACA 252
                                                                                                                                                                                                                                                                                           313 CTATGGAAAGAAGCTGATCGGCTGTCTGTGCATCGAACACAAGAAGTACAGCCGCA 372
                                                                                                                                                                                                                                                                                                                                                          373 ATGCTCTCCTCTTCAACCTGGGCTTCGTGTGTGATGCCCAGGCCAAGACCTGCGCCCTCG 432
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                                                                                                                                                                                                         37 ThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGln 56
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                                                                                    6 TyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGlu
                                                                                                                                                                                                                                                                                                                            71 AlaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSer
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                                                                                                                                                   ---LysAsnSerSerAlaAsn----LeuThr
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 313, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: NUCLEIC Acids, Proteins and Antibodies
FILE REFERENCE: PA103PIC1
CURRENT APLICATION NUMBER: US/10/102,806
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
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Matches:
Conservative:
Mismatches:
Indels:
                                                          US-10-048-196-2 (1-134) x US-09-918-995-28770 (1-454)
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 Mismatches:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 313
LENGTH: 4106
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71.50
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Best Local Similarity:
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Best Local Similarity:
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US-10-102-806-313
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               Query Match:
DB:
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Buu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPIJ300-3
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-06
PRIOR FILING DATE: 2001-01-06
PRIOR FILING DATE: 2001-01-16
SEQ ID NOS: 5379
LENGTH: 768
                                                                                                                                                                                                                                                                                  1071 CAAGACACAGTGTCAGAACCAGTCACACCTGCATCTTTGCTGCTTTACAGAGTGATGTG 1130
                                                                                                                                                                                                       963 GGTGGTAATAAGCTGCAGTCAACAGGAAATAAAGCAGAAGAACACAAAAGGAACCGAATGT 1022
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903 TCAGCAGTGCCTACAAATATGGCTGCCAAGAAAACATCTACCCCCAAAATTTTGTT
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                                                                    AlaAlaMetLysLeuSerSerGluSerLysAla----
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Matches:
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Arabidopsis thaliana US-09-938-842A-812
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Best Local Similarity:
Query Match:
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Oy . 109 nLysIleValargHisSerLeuLysProCysMetLeuGluThrValasnalaPhe 127 	RESULT 29 US-09-880-107-2249/c ; Sequence 2249, Application US/09880107 ; Patent No. US20020142981A1 ; GENERAL INPORMATION: ; APPLICANT: Horne, Darci T. ; APPLICANT: Scherf, Uwe	APPLICANT: TITLE OF INTITLE OF IN	; SEQ ID NO 2249 ; LENTH: 2267 ; TYPE: DNA ; ORGANISM: Homo sapiens ; CEATURE: ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M13143 US-09-880-107-2249	Alignment Scores: 6.93 Length: 2267 Pred. No.: 71.00 Matches: 28 Score: 71.00 Matches: 26 Percent Similarity: 38.38 Conservative: 26 Best Local Similarity: 20.14% Mismatches: 50 Query Match: 10.50% Indels: 35 DB: 4	US-10-048-196-2 (1-134) x US-09-880-107-2249 (1-2267) QY 20 CysalaSerThrPro-GluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLe 39	1372 GGTGTCCTATGAGTGACCCTCCACAGGTGCCTCTGAGCTGTCAGCTTCACCTGCAGGC	Oy 54 yHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSe 74	Qy 74 rGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLe 94 	Qy 94 uThrThrAlaAla	OY 106GluvalAlaGl 109 Db . 1144 ATCTTAAGAAACACTTACACTTCTCTTACAGTTATGGGAGTAAAGAATAAGTGA 1085	Oy 109 nLysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnAlaPhe 127 :::: :::::::::: ::::::::: ::::::	RESULT 30 US-09-729-920-3/c ; Sequence 3, Application US/09729920
bb 597 AGCTCCACCTCCTGCTAACCACCACCATGAGCTCCTTCGCCAGAACCTCCTCC 538 Oy 87 GlualaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGlu 106	Db 537 TCCACCCCCACCATTCCACCACCACCACCTCCTCCCCCGGCACCTCCACCTCC 478 Qy 107 ValalaGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnala 126 :::::	PB 432 ACCATGTGCACCACCACCACCACC 412 RESULT 28 US-09-964-824A-248/C : Sequence 248, Application US/09964824A : Sequence 248, Application US/09964824A : Patent US20020102531A1 : Patent INFORMATION: : APPLICANT: Horrigan, Stephen : TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu : TITLE OF INVENTION: Sets : FILE REFERENCE: 689290-73	CURRENT APPLICATION NUMBER: US/03/964,824A CURRENT FILING DATE: 2001-09-27 PRIOR APPLICATION NUMBER: US/60/236,033 PRIOR APPLICATION NUMBER: US/60/236,032 PRIOR FILING DATE: 2000-09-28 PRIOR FILING DATE: 2000-09-28 PRIOR FILING DATE: 2000-09-28 PRIOR FILING DATE: 2000-09-28 PRIOR FILING DATE: 2000-09-28	NUMBER OF SEQ ID NOS: 583 SOFTWARE: Patentin version 3.0 SEQ ID NO 248 LENGTI 2267 TYPE: DNA ORGANISM: Homo sapiens US-09-964-824A-248	Alignment Scores: 6.93 Length: 2267 Pred. No.: 71.00 Matches: 28 Score: 38.85\$ Conservative: 26 Best Local Similarity: 20.14\$ Mismatches: 50 Query Match: 10.50\$ Indels: 35 DB:	-10-048-196-2 (1-134) x US-09-964-824A-248 (1-2267)	Qy 20 CysAlaSerThrPro-GluSerAsnProLysAsnSerSerSerAlaAsnLeuThrThrSerLe 39	Qy 39 ulleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGl 54 1:: :::	Oy 54 yHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSe 74	Oy 74 rGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLe 94 Db 1260TGTGTTTTTGTTGTGAGACAGAGTTGTCCCCAGTGTTACACAATCTCAAAG 1205	Oy 94 uThrThralaala105	Oy 106GluValalaGl 109 Db 1144 ATCTTAAGAAACACTTACACTTCCTTACAGTCTTCTGGGAGTAAAGAATAAGTGA 1085

us-10-048-196-2.rnpb

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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica -x -
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69. CCGGTGAGCCGCGAGAGAGAGGGCGCGCATCCTCGCAGGTCGCCCCTCGTCG 128
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                                                                                                                                                                                                                                                                                                              ----AlaSerThrProGluSerAsnProLysAsnSerSer
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Mismatches:
Indels:
    ; OTHER INFORMATION: wherein any n is one of a or US-09-867-550-61
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Matches:
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-36
PRIOR PELICATION NUMBER: US 09/632,366
PRIOR PELICATION NUMBER: US 036,359
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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70.50
41.82%
26.36%
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Best Local Similarity:
Query Match:
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APPLICANT: Colley, Pamela
APPLICANT: Colley, Pamela
APPLICANT: Colley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR FILING DATE: 2000-05-30
             GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLBIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000858

CURRENT APPLICATION NUMBER: US/09/729,920

CURRENT FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FASISEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57503 CAACGTACCCGCAGTGCAAGCCCAGCTGTGAGAGATCAGGGCAGCAGCAGGCCCTGATC 57444
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
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10.50%
Patent No. US20020103115A1
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LOCATION: (1)
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                             LENGTH: 143306
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LENGTH: 455
                                                                                                                                                                                                                                      SEQ ID NO 3
                                                                                                                                                                                                                                                                                   TYPE: DNA
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Patent No. US20020091244A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 ACACCTACATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACTGAGGGCCTCTGG 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 ValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXPRESSED IN HELA, SIGNAL = 4.4

EXPRESSED IN HELA, SIGNAL = 4.4

EXPRESSED IN PLACENTA, SIGNAL = 4.3

EXPRESSED IN BRAIN, SIGNAL = 1.8

EXPRESSED IN LUNG, SIGNAL = 3.3

EXPRESSED IN HERAT, SIGNAL = 1.9

EXPRESSED IN HERAT, SIGNAL = 1.9

EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 uLysProCysMetLeuGluThrValAsnAlaPhelleValPro 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 GCCACCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCC 209
                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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Matches:
Conservative:
Mismatches:
Indels:
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                                                          PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
PCT/US01/00663
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US-09-799-777-112
; Sequence 112, Application US/0979777
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAP TO Z82188.2
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70.50
42.22%
26.67%
10.43%
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: M.
CTHER INFORMATION: E.
COTHER INFORMATION: E.
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Best Local Similarity:
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LENGTH: 980
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529 ---AGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTCATCCTGTACGCGCAGC 685
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                                                                                Baugh, Mariah
Sather, Susan
Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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36
21
56
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Mismatches:
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STREET: 3174 PORTER DRIVE
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Matches:
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APPLICATION NUMBER: US/09/002,485
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/799,777
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                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                      Hillman, Jennifer L. Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: PROSNOT20
                                                                                                                                                                                                                                                                               STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                       CORRESPONDENCE ADDRESS
APPLICANT: Lal, Preeti
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26.67%
10.43%
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                                                                Guegler,
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                         ZIP: 94304
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Db 911	Qy 44 ValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysTleAlaAlaMet 63 :::::	Qy 64 LysLeuSerSerGluSerLysAlaLysIleSerGluThr 76	Oy 77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThr 96	9 y AlaAlaIlesinPichandlahrqfhichtvalladibysile-valArgibiserle 116 1187 ACACCHAACCTACACTTCAGCCCACCTACTAGGCCCAGGAGGCTGGG 118 1187 GCCACCTCCGGCGGCAGGCCACCTACTAGGCCCAGGAGGCTGGGGGGGCTGGGGGGGG	APPLICATION N FILING DATE: APPLICATION N
Db 686 CCAGCGAGCGCAGCATGATGCAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGGACC 745	Oy 77 AlaCysGlyCysValalaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThr 96	Qy 97 AlaalaIleAsnProAsnalaArgThrGluValAlaGlnLysIle-ValArgHisSerLe 116 11 1 1 1 1 1 1 1 1 1	Oy 116 uLysProCysMetLeuGluThrValAsnAlaPheIleValPro 130	Section Sect	24 ProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla

998-6998-699998-699998-6999998-69999	06-04 78: 60/08802 78: 60/08803 78: 60/08803 78: 60/08803 78: 60/08803 78: 60/08803 78: 60/08820 78: 60/08820	23.40
DATE: ATION	LING DATE: DLICATION LING DATE: PLICATION LING DATE: LING DATE: LING DATE: LING DATE: LING DATE: LING DATE: PLICATION LING DATE: PLICATION LING DATE: LI	ILLING DATE: ILLING DATE: ILLING DATE: ILLING DATE: ILLING DATE: PPLICATION ILLING DATE: ILLING DATE: PPLICATION ILLING DATE: PRICATION
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PRIOR APPLICATION NUMBER: 60/089653
PRIOR PILLICA DATE: 1998-06-18
PRIOR PILLICA DATE: 1998-06-18
PRIOR PILLICA DATE: 1998-06-18
PRIOR PILLICATION NUMBER: 60/08907
PRIOR APPLICATION NUMBER: 60/08947
PRIOR PILLICATION NUMBER: 60/08947
PRIOR PILLICATION NUMBER: 60/08948
PRIOR PILLICATION NUMBER: 60/09045
PRIOR PILLICATION NUMBER: 60/09045
PRIOR PILLICATION NUMBER: 60/09045
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PRIOR PILLICATION NUMBER: 60/09044
PRIOR PILLICATION NUMBER: 60/09045
PRIOR PILLICATION NUMBER: 60/09045
PRIOR PILLICATION NUMBER: 60/09046
PRIOR PILLICATION NUMBER: 60/09065
PRIOR PILLICATION NUMBER: 60/09065
PRIOR PILLICATION NUMBER: 60/09069
PRIOR PILLICATION NUMBER: 6

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1002 ACACCTACATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACTGAGGGCCTCTGG 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 AlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIle-ValArgHisSerLe 116
                                                                                                                                                                                                                                                                                                                726 ACCTTGATGGGTGCTTTGACATGGCGACCGGCCAGTTTGCTGCTCCCCTGCGTGGCATCT 785
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825 ---AGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTCATCCTGTACGCGCAGC 881
                                                                                                                                                                                                                                                                                                                                                 24 ProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 LysLeuSerSerGluSer---LysAlaLysIle------SerGluThr 76
                                                                                                                                                                                                                                                                               10 ThrLeuMetThrAlaPheThr-------LeuAlaSerCysAlaSerThr 23
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                                                                                                                                                                                                                                                                                                                                                                     44 ValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  882 CCAGGGAGCATCATGCAGAGCCAGAGTGTGTATGCTGGACCTGGCCTACGGGACC
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                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grimaldi,J.Christopher
Gurney,Austin L.
Kljavin,Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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tewart, Timothy A
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Goddard, Audrey
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70.50
42.22%
26.67%
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Botstein, David
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                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                        Alignment Scores
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                                                                                                                          Pred. No.:
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                                                                                                                                              Score:
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secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same TILLE OF INVENTION: SCI-GE CONDING THE SAME
CURRENT APPLICATION INDRER: 05/04/991, 293A
CURRENT FILING DATE: 1001-11-20
CURRENT FILING DATE: 1001-11-20
PRIOR FILING DATE: 1001-06-16
PRIOR PRILING DATE: 1001-06-16
PRIOR PRILING DATE: 1001-06-16
PRIOR PRILING DATE: 1001-06-16
PRIOR PRILING DATE: 1001-06-17
PRIOR PRILING

NUMBER: 60/088861 1998-06-11 NUMBER: 60/089105 1998-06-12 NUMBER: 60/089105 1998-06-16 NUMBER: 60/089514 1998-06-16 NUMBER: 60/089533 1998-06-17 NUMBER: 60/089538 1998-06-17 NUMBER: 60/089590 1998-06-17 NUMBER: 60/08990 1998-06-17 NUMBER: 60/08990 1998-06-17 NUMBER: 60/08990 1998-06-19 NUMBER: 60/08990 1998-06-19 NUMBER: 60/08990 1998-06-19 NUMBER: 60/08990 1998-06-19 NUMBER: 60/08990 1998-06-19 NUMBER: 60/08990 1998-06-19 NUMBER: 60/08990 1998-06-19 NUMBER: 60/08990 1998-06-19 NUMBER: 60/08055 1998-06-19 NUMBER: 60/09025 1998-06-19 NUMBER: 60/09025 1998-06-22 NUMBER: 60/09025 1998-06-23 NUMBER: 60/09025 1998-06-23 NUMBER: 60/09035 1998-06-23 NUMBER: 60/09035 1998-06-23 NUMBER: 60/09043 NUMBER: 60/09043 NUMBER: 60/09043 NUMBER: 60/09043 NUMBER: 60/09043 NUMBER: 60/09043 NUMBER: 60/09043 NUMBER: 60/09043	NUMBER: 1998-06 NUMBER: 1998-0
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Matches:
Conservative:
Mismatches:
Indels: US-10-048-196-2 (1-134) x US-09-989-293A-46 (1-3089) PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091869
PRIOR PILING DATE: 1998-07-01
PRIOR PAPLICATION NUMBER: 60/091360
PRIOR PELING DATE: 1998-07-01
PRIOR PAPLICATION NUMBER: 60/091549
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/09159
PRIOR PAPLICATION NUMBER: 60/091626
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PRIOR APPLICATION NUMBER: 60/091639
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091639
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091639
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182 US-05-989-735-46
Sequence 46, Application US/0989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P. 13.3 70.50 42.22% 26.67% 10.43% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: .. 9 64 ŏ g ōλ g δ qq Qγ g g ŏ

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R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R FILING DATE: 1998-06-09
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R FILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/089105

R APPLICATION NUMBER: 60/089105

R FILING DATE: 1998-06-12

R APPLICATION NUMBER: 60/089440

R FILING DATE: 1998-06-16
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R APPLICATION NUMBER: 60/08598

R FILING DATE: 1998-06-17

R FILING DATE: 1998-06-17

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089600

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089653

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089653
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R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089952
R APPLICATION NUMBER: 60/090246
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R FILING DATE: 1998-06-22
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/090355
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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60/088202
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 6
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APPLICATION NUMBER:
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CURRENT APPLICATION WUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
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APPLICATION NUMBER: 60/075945
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PLICATION NUMBER: 60/078910
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PLICATION NUMBER: 60/084600
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/087827
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Williams, P. Mickey
Wood, William I.
                                                                Perrara, Napoleone
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tewart, Timothy
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                                                                                                                                  Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                  aoni, Nicholas F
                                                                                                             Gerber, Hanspeter
                                                                                                                                                                                                                          Gurney, Austin L
                                                                                                                                                                                                                                                    ljavin, Ivar J
                       Desnoyers, Luc
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                                                                                                                                                                                  Godowski, Paul
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PIC19
CURRENT APPLICATION NUMBER: US/09/990,444
PRIOR APPLICATION NUMBER: 60/09787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
                                                                                                                                           97 AlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIle-ValArgHisSerLe 116
    882 CCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGGTGGACCTGGCCTACGGGGACC 941
                                                              77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThr 96
                                                                                                                                                                                                                                                                  1062 GCCACCCTCCCGGCTGGAGCTCAGGTGCTGGTCCCGTCCCC 1104
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RAPELICATION NUMBER: 60/065186

RELING DATE: 1997-11-12

RAPELICATION NUMBER: 60/065311

RELING DATE: 1997-11-3

RAPELICATION NUMBER: 60/065710

RAPELICATION NUMBER: 60/06770

RELING DATE: 1997-11-24

RAPELICATION NUMBER: 60/075945

RELING DATE: 1998-02-25

RELING DATE: 1998-03-20

RAPELICATION NUMBER: 60/083322

RELING DATE: 1998-04-28

RELING DATE: 1998-06-07

REPLING DATE: 1998-06-07

REPLING DATE: 1998-06-07
                                                                                                                                                                                                                                                                                                                                             Sequence 46, Application US/09990444 Publication No. US20020193300A1 GENERAL INFORMATION:
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Stewart, Timothy A.
Tumas, Daniel
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Goddard, Audrey
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Botstein, David
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R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091978
R APPLICATION NUMBER: 60/091982
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R APPLICATION NUMBER: 60/09187
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R FILING DATE: 1998-07-07
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R FILING DATE: 1998-07-02
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; Sequence 46, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-06-16
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
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Botstein, David
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R FILING DATE: 1998-02-25
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APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088738 PILING DATE: 1998-06-10 APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-12 PPLICATION NUMBER: 60/065186 ILING DATE: 1997-11-12 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 'ILING DATE: 1998-04-28 PPLICATION NUMBER: 60/084600 ILING DATE: 1998-06-04 PPLICATION NUMBER: 60/088025 FLING DATE: 1998-06-04 PPLICATION NUMBER: 60/088026 PPLICATION NUMBER: 60/088033 ILING DATE: 1998-06-04
PPLICATION NUMBER: 60/088167 PPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 TLING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861 PPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/089440 PPLICATION NUMBER: 60/065311 PPLICATION NUMBER: 60/087609 PPLICATION NUMBER: 60/087759 PPLICATION NUMBER: 60/087827 ILING DATE: 1998-06-03 PPLICATION NUMBER: 60/088021 PPLICATION NUMBER: 60/088028 PPLICATION NUMBER: 60/088029 PPLICATION NUMBER: 60/088326 PPLICATION NUMBER: 60/088202 PPLICATION NUMBER: 60/088742 PPLICATION NUMBER: 60/088810 ILING DATE: 1998-06-10 PPLICATION NUMBER: 60/088824 LING DATE: 1998-06-10 LING DATE: 1998-03-20 998-06-02 1998-06-02 ILING DATE: 1998-06-05 LING DATE: 1998-06-04 998-06-10 998-06-04 1998-06-04 1998-06-11 0-90-866 LING DATE: LING DATE: LING DATE: LING DATE: ILING DATE:

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LICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/090431
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Matches:
Conservative:
Mismatches:
Indels: US-10-048-196-2 (1-134) x US-09-989-730-46 (1-3089) Gaps: 10 ThrLeuMetThrAlaPheThr------R APPLICATION NUMBER: 60/091478
R FILING DATE: 1998-07-02
R FILING DATE: 1998-07-01
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-02
R FILING DATE: 1998-07-02 R FILING DATE: 1998-07-02
R PAPLICATION NUMBER: 60/091978
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/092182
R FILING DATE: 1998-07-09 Sequence 46, Application US/09990436 Publication No. US20020198148A1 GENERAL INFORMATION: Ferrara, Napoleone Fong, Sherman 998-07-0 Gerber, Hanspeter Gerritsen, Mary E 13.3 70.50 42.22% 26.67% APPLICANT: Ashkenazi, Avi J Baker, Kevin P. Botstein, David Desnoyers, Luc Eaton, Dan Percent Similarity: Best Local Similarity: US-09-990-436-46 Alignment Scores Query Match: Pred. No.: PRIOR
PRIOR RESULT 40 Score: ð ð ò

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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
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R APPLICATION NUMBER: 60/088026

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APPLICATION NUMBER: 60/088025
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PPLICATION NUMBER: 60/065186
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PPLICATION NUMBER: 60/065311
ILING DATE: 1997-11-13
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LICATION NUMBER: 60/075945
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
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LING DATE: 1998-05-28
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APPLICATION NUMBER: 60/088655
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Grimaldi,J.Christopher
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                           Roy, Margaret Ann
Stewart, Timothy A
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                rney, Austin
                                             Napier, Mary A.
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R FILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091544
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/090557
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/090535
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US-10-048-196-2 (1-134) x US-09-990-436-46 (1-3089)

10 ThrLeumetThralaPheThr	24 ProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla 43 	44 VallysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIlealaalaMet 63 ::::: :::	64 LysLeuSerSerGluSerLysAlaLysIleSerGluThr 76	77 AlacysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThr 96
10 ThrLeuMetThralaPheThr 	ProGluSerAsnProLysAs	ValLysGlnThrCysGlnTh :::::: AGACGTACGTGCACTT	LysLeuSerSerGluSer ::: CAGCGAGCGCAGCATCATG	AlacysGlycysValAlaAspLysAla
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97 AlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIle-ValArgHisSerLe 116
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116 uLysProCysMetLeuGluThrValAsnAlaPheIleValPro 130

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Search completed: May 5, 2003, 23:56:37 Job time : 128 secs

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5, 2003, 22:18:19 ; Search time 1060 Seconds (without alignments) 2047.354 Million cell updates/sec
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	AQ886059 476 bp DNA linear GSS 09-NOV-1999	HS_5530_B2_C07_SP6E RPCI-11 Human Male BAC Library Homo sapiens	genomic clone Plate=9298 Col=14 Row=F, DNA sequence.	AQ886059	AQ886059.1 GI:6317526	GSS.	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 476)	Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,	Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
AQ886059/c	rocns	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	

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em_gss_fun:*

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em_gss_hum:* em_gss_pln:* em_gss_vrt:* em_gss_mam:* em_gss_mus:*

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Triticum aestivum
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80 AAT 78
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                                                          Loundact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3819
Fax: (206) 616-387
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector EcoRI sites" 3 others
               A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 TTAAGGCTGATGATCACAGCCACAGTAATGCNACTGTCTTCAGCAGCACACATAGAACTG 381
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380 ACACATGGCATGGGTCAGAGTGGAATATGCAGGAAGTCATGCATTGACATTCCTCATCTG 321
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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source 1709 /organism="Triticum /cultivar="Butte 86"	/db.xrei="taxon:4565" /clone="WHE3559 G01] /clone_lib="Wheat de" /tissue_type="whole of dev_stage="3-44 day /lab_host="E. coli \$ /note="Vector: Lambd ECORI; Plants were g environmental regime	240C/170C day/night, fertilizer, Environm well-watered, withou Environment 3) 370C/ post-anthesis fertil day/night, well-wate Environment 5) 370C/ Environment 5) 370C/ Environment 5) 370C/	day/night plus droug developing wheat gra and frozen in liquid 8, 10, 12, 16, 20, 2 at 3, 5, 7, 8, 10, 10a Barizonment 3 at 10ba Barizonment 3 at 10 Barizonment 3 at	20, 24, 28, 30 DPA Environment, 28, 32, 34 DPA Environment, 20, 24, 28, 30 DPA Environment, 20, 24, 28, 30 DPA Environment, 20, 24, 28, 30 DPA Environment, 20, 20, 24, 28, 30 DPA Environment, 20, 20, 20, 20, 20, 20, 20, 20, 20, 20	ONIME 23.1 S	cores:	Pred. No.: Core:, 0.532 Le Score:, 94.50 Ma Percent Similarity: 37.96% Co Best Local Similarity: 25.55% Mi Query Match: 13.98% In DB: 14	US-10-048-196-2 (1-134) x BQ804850 (1-709 Qy 7 ValThrAlaThrLeuMetThrAlaPheThrL	27	Qy 47 ThrCysGlnThrGlnLeuThrGlyHisGlnT 	301 75	DB 351 GCAGTGCCAGGCCATCCAAAATGTTGTTCAT Qy 90 SerLeuThrGluLeuThrThrAlaAlaIleA
BASE COUNT 276 a 258 c 126 g 153 t ORIGIN	s: 0.699 95.00 41.738 Larity: 25.908 14.058	US-10-048-196-2 (1-134) x BQ839107 (1-813) QY 7 ValThralaThrLeuMetThralaPheThrLeuAlaSerCysAlaSerThrProGluSer 26 QY 7 ValThralaThrLeuMetThralaPheThrLeuAlaSerCysAlaSerThrProGluSer 26 Ill::: ::: ::: Db 336 GTATCGGCAACCACAACAACTATTCGCAGCAACAACAACAACAACAACAACAACA 395 QY 27 ASPPROLYSASDSErSERALAASDLEUTHTHRSErLEUIIELYSHisAlaValLySGln 46 :::	TCAACAAATTCTGCAACAACAGATTCCATGG GlnThrGlnLeuThrGlyHisGlnTyrTrpLysIlealaalaMet :::	Qy 65 LeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys 84		Qy 108 AlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnala 126 :::		ACCESSION BQ804850.1 GI:22029059 KEYWORDS EST. SOURCE bread wheat. ORGANISM Triticum eestivum ORGANISM Triticum eestivum	<pre>Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum. REFERENCE 1 (bases 1 to 709) . AUTHORS Altenbach, S., Anderson, O. D., Chao, S., Chin, A., Close, T.J., Cronin , K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J.,</pre>	Wilson,C. and Woo,J. TITLE The structure and function of the expressed portion of the wheat genomes - Developing grains cDNA library JOURNAL Unpublished (2002)		Email: oandersnepw.usda.gov Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: SK primer. FEATURES FEATURES

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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
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Altenbach.S., Anderson.O.D., Chao.S., Chin,A., Close,T.J., Cronin,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J., Wilson,C. and Woo,J.

The structure and function of the expressed portion of the wheat genomes - Developing grains cDNA library
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Fax: 5105595818
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/cultivar="Butte 86"
/dutivar="Butte 86"
/dutivar="Butte 86"
/dutivar="Butte 86"
/dutivar="Souri-4565"
/clone=lib="Wheat developing grains cDNA library"
/tissuc_type="whole grains"
/dev_stage="3-44 days post anthesis seed"
/lab_host="E. coli SOLR"
/note="Vector: Lambda ZAP II, excised phagemid; Site_1:
ECORI; Plants: were grown under six following different
environmental regimes in greenhouse, Environment 1)
240c/l7oc day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 240c/l7oc day/night,
well-watered, without post-anthesis fertilizer,
Environment 3 370c/l7oc day/night, well-watered, with
post-anthesis fertilizer, Environment 4) 370c/l7oc
day/night, well-watered, without post-anthesis fertilizer,
Environment 5) 370c/l7oc day/night blus drought, with
post-anthesis fertilizer, Environment 6) 370c/l7oc
day/night plus drought, without post-anthesis fertilizer,
Environment 5) 370c/l7oc, day/night plus drought, without post-anthesis fertilizer,
Environment 6) 370c/l7oc, day/night plus drought, without post-anthesis fertilizer,
Environment 1 2, 370c/l7oc, day/night blus drought, without post-anthesis fertilizer,
Day/night plus drought, without post-anthesis fertilizer,
developing wheat grains from the following were excitized
and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,
8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S.
Altenbach and R. Cronin at USDA-ARS, Albany, CA. A CDNA
library was made using poly (A) RNA, and and the cDNA clones
were in vivo excised to give pallescript SRC-) phagemids
in the TJ Close lab (Chin, 
                                                                                                                                                                                                                                                                                                            EST 31-JUL-2002
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WHE3552_CO6_E12ZS Wheat developing grains cDNA library Triticum
aestivum cDNA clone WHE3552_CO6_E12; mRNA sequence.
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                                110 LysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnAla 126
                                                                                   466 ACAATA-----TCCATTAGGCCAGGCTCCTTCCGGCCATCTAGCA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: oandersn@pw.usda.gov
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Fax: 5105595818
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1080 bp mRNA linear EST 05-MAR-2002
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1...1000
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5581015"
/clone_Lib="NIH_MGC_67"
/clone_Lipe="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6 Site_1: NotI;
/note="SalI; Cloned unidirectionally."
//organism="SalI; Cloned unidirectionally."
//organism="SalI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12340 row: d column: 08

High quality sequence stop: 740.
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   110 LysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnAla 126
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Mismatches:
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Best Local Similarity:
Query Match:
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                                                                                                             /clone_1hp="Wheat developing grains cDNA library"
/clone_1hp="Wheat developing grains cDNA library"
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/lab_host="E. coli $Scir"
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/lab_host="Environment 2"
/lab_host="Environment 2"
/lab_host="Environment 4"
/lab_host="Environment 4"
/lab_host="Environment 4"
/lab_host="Environment 5"
/lab_host="Environment 6"
/lab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472 GGATGTTGTATTGCAGCAACACATAGCGCATGGAAGATCACAAGTTTTGCAACAAAG 531
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532 TACTTACCAGCTATTGCAATTGTGTTGTCAGCACCTATGGCAGATCCCTGAGCAGTC 591
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Conservative:
Mismatches:
Indels:
/organism="Triticum aestivum"
/cultivar="Butte 86"
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AW504179 427 bp mRNA linear EST 02-MAR-2000 UI-HF-BNO-ale-f-08-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079431 5', mRNA sequence.
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Eukaryota; Metzoos; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 427)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collegtion (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
      282.ACTCCAGGCCAAGCTC----CACCTCGCCTGGAAATGGTTATCTCCTGAATCCGGCA 335
                                                                                                                                                                                                                                                                              396 CCAGCAGAACAGCTCCAAACAGATGGCTGCACCAGCAACAAAGGGCCCAAACTCATGCAG 455
                                                                                                                                                     336 GCAGTGACAGTGGCCGGTTCAGCGTCAGGGCCTGTGGCTGTGCCCAGCTCTGACATGTCT
                                                                                                                                                                                                                  -----ValAlaAspLys-----
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                                                                                                                                                                                                                                                                                                                                           86 roGluAlaValSerLeuThrGluLeuThrThrAlaAla 98
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AW504179
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submitssion
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chanical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-509-9170,
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                              09-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-023L05.TJ.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
:: ::: 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 |
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BAC end sequences of Library RPCI-43
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
231 c 137 g 129 t
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R.Site 2 : ECORI
Location/Qualifiers
1 . 679
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AGI58466.1 GI:16688144
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/cell_type="garmina" center B cells"
/cell_line="MGC85"
/lab_bost="DHIOB (LTI)"
/lab_bost="DHIOB (LTI)"
/note="Vector: pT713-Pac; Site_l: Not!; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4 4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
154 c 95 g 88 t
Email: cgapbs-rémail.nih.gov

Eco RI site shown at the bequinning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D. Ph.D.

CDNA Library Preparation: M.B. Soares Lab.

CDNA Library Arrayed by: M.B. Soares Lab.

DNA Sequencing by: M.B. Soares Lab.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbry/image.html

Seq primer: MI3 Porward.
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Matches:
                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:3079431"
/clone_lib="NIH_MGC_50"
/tissue_type="lymph"
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                                                                                                                                                                                                                                                                                   Location/Qualifiers
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BASE COUNT 18 ORIGIN	Alignment Scores: Pred. No.: Score:	Percent Similarity Best Local Similar Query Match:	. US-10-048-196-2 (1	Oy 1 MetMetLy	63	Qy 21 AlaSerTh	Db 123 ATATICIC	Oy 38 SerLeuIl ::: Db 183 ACTTTGAT	Qy 48Cy	8	. Oy 56	Db 303 TTCTTA	363	Qy 83 ASPLYSA	Db 411	Qy 103 AlaArgTh	Db 456	Qy 123 ThrvalAs	Db 501 TTGGTAAA		ISM CE RS AL	COMMENT CONTECTION COLLUI Heinri Martin FEATURES SOURCE
Oy 28 ProLysAsnSerSerAlaAsn-LeuThrThrSerLeuIleLysHisAlaValLysGlnTh 47	47 rCysGlnThrGlnLeuThrGlyHis-GlnTyrTrpLysIleAlaAlaMetLysLeuSers	Db 273 ACTCCAGGCCAAGCTCCACCTCGGCCTGGAATGGTTATCTCCTGAATCCGGCA 326 Oy 67 erGluSerLysAlaLysIleSerGluThrAlaCysGlyCys 80	327	r 694	LOCUS A2358694 679 bp DNA linear GSS 02-OCT-2000 DEFINITION INDIOINIPIP MOUSELINE MOUSELINE MOUSELINE MOUSELINE MOUSELINE MOUSELINE MOUSELINE MOUSELINE MOUSELINE GROWN FOR THE OFFICE MOUSE MOUSELINE MOUSELI	ACCESSION A2358694 VERSION A2358694.1 GI:10472394	S GSS. house mouse.	_ 	<pre>REFERENCE 1 (bases 1 to 6/9) AUTHORS Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly</pre>			JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss This parests of the bound Contex	University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT	84112, USA Tel: 801.585 5606	Fax: 001 303 /1// Email: ddunn@dannts.utah.edu Tmeart Iannth: 1000 ctd Bryn: 0 00		Class: plasmid ends Class: plasmid ends	FEATURES 11gh quality Sequence Stop: 0/9. FEATURES 1 Location/Qualifiers 1 570		/db_xref="taxon:10090" /clone="UUGCIM0101B17" /clone_lib="Mouse lobb plasmid UUGCIM library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource	(nt.p.//www.lax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel	electrophoresis. Vector UNA was prepared iron a derivative of pWD42 (qi14732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purifited. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

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sulus gallus
sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
rrchosauria; Aves; Neognathae; Galliformes; Phasianidae;
hasianinae; Gallus.
(bases 1 to 811)
suerstedde, J.M.
sulus gallus bursal lymphocyte EST
solutat: Buerstedde JM
cellular Immunology
eleintich-PetterInstitute
faintich-PetterInstitute
faintich-PetterInstitute
fartinistr. 52, 20251 Hamburg, Germany
Location/Qualifiers
1. 811
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and selected for ampicillin resistance." 86 a 147 c 102~\mathrm{g} 244~\mathrm{t}
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Eukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
; Triticeae; Triticum.
Clarke, B., Lambrecht, M. and Rhee, S.
Assessing the utility of Arabidopsis genomic information for Interpreting wheat EST sequences
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ606191 630 bp mRNA linear EST 25-JUN-2002 BRY_2034 wheat EST endosperm library Triticum aestivum cDNA 5', mRNA sequence.
BQ606191.1 GI:21555417
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                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
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437 GTTGAGCCAACTCTTCCAACAGCCTCAGCAACAATA------TCCATCAGGCCA 487
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Indels:
                                           /organism="Triticum aestivum"
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Db 444 GATCCTTCAACAAATTTGCAACAACTGATTCCATG	11 71 SULT 1 804628 804628 CUS FINITI FINITI CESSIO RSION FWORDS URGE	Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae ; Trittcae; Trittcum. ; Trittcae; Trittcum. ; Trittcae; Trittcum. ; Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J., Cronin , K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J., Wilson,C. and Woo,J. TITLE The structure and function of the expressed portion of the wheat genomes. Developing grains cDNA library JOURNAL Unpublished (2002) COMMENT US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 510559578 Fax: 5105595818 Email: oandersn@pw.usda.gov Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Sequences have been trimmed to remove vector sequence and low guality sequence with phred score less than 20 Sequences have been trimmed to remove vector sequence and low guality sequence with phred score less than 20 Sequences have been trimmed to remove vector sequence and low guality sequence with phred score less than 20 Sequences have been trimmed to remove vector sequence and low guality sequence with phred score less than 20 Sequences have been trimmed to remove vector sequence and low guality sequence with phred score less than 20 Sequences have been trimmed to sequence and low sequence with phred score less than 20	Con
AUTHORS Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin, K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J. Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J. and Wool, T.D. Lazo, G.R., Pham, J., Rausch, C.J., Millon, C.J., Cronin The structure and function of the expressed portion of the wheat genomes - Developing grains cDNA library Contact: Olin Anderson Grains cDNA library Unpublished (2002) GOMENT Contact: Olin Anderson Us Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595818 Email: oandersn@pw.usda.gov Sequences have been trimmed to remove vector sequence and low guality sequence with phred score less than 20 Sequences Sequence with phred score less than 20 Sequences Sequence Milliers Sequence Milliers	source 1. 787 /crganism="Triticum aestivum" /cultivar="Butte 86" /db_xref="taxon:4565" /clone="WHE3586_AOV_Bal4" /clone="WHE3586_AOV_Bal4" /clone="WHE3586_AOV_Bal4" /tissue_type="whole grains" /de_stage="3-44 days post anthesis seed" /lab_host="E. coli SolE" /note="Vector: Lambda ZAP II, excised phagemid; Site_1: ECORI; Plants were grown under six following different environmental regimes in greenhouse, Environment 1) 24oC/17oC day/night, wall-watered, with post-anthesis fertilizer, Environment 2) 24oC/17oC day/night, well-watered, without post-anthesis fertilizer, Environment 3) 37oC/17oC day/night, well-watered, with	post-anthesis fertilizer, Environment 4) 370C/170C day/night, well-watered, without post-anthesis fertilizer, Environment 5) 370C/170C day/night plus drought, with post-anthesis fertilizer, Environment 6) 370C/170C day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 32, 34, 32, 34 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 30, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 30, 24, 28, 30 DPA and total RNA was prepared by S. Altenbach and K. Cronin at USDA-RRS, Albany, CA. A CDNA library was made using poly (A) RNA, and the cDNA clones were in vivo excised to give pBluescript SK(') phagemids in the TJ Close lab (chin, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD	

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119 CysMetLeuGluThrValAsnAla 126
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/clone_lib_argory wh_e".
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/dev_stage="Feekes" scale 11.2"
/note="Wector: Lambda Uni-ZAP XR, excised phagemid;
Site_l: EcoRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the CDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
/ Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 -----CAGGGATGTTGTATTGCAACAACACATAGCGCATGGAAGCTCACAAGT 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 -----SerGluSerLysAla 71
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Ontact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fal: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                /cultivar="Chinese Spring"
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89.50
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Wheat functional genomics - Glenlea developing seeds cDNA libraries Wheat functional (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe RG, Winnipeg, MB, Canada R3T 2M9
Fax: (204) 983-2140
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
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Site_1: NoII; Site_2: Mlu1; mRNA obtained from wheat seeds
of cultivar Glass post-anthesis"
204 c 115 g 134 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ246193 671 bp mRNA linear EST 03-MAY-2002
TaE15015A03R TaE15 Triticum aestivum cDNA clone TaE15015A03R, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: scloutierem.agr.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >1.4 kb
Plate: 015 row: A column: 03
Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                              284 ------TATTCTGCATCAACAAAAAACAACAACAACAACCATCGAGCCA 328
                                                                                                                                ------CATGGATGTTGTATTGCAGCAACACATAGCGCATGG 163
                                                                                                                                                                                                                              164 AAGATCACAAGTTTTGCAACAAAGTACTTACCAGCTGTTGCAAGAATTGTGTGTCAGCA 223
                                                                                                                                                                                                                                                                                                                        224 CCTATGGCAGATCCCTGAGCAGTCGCAGTGTCAGGCCATCCAAAATGTTGTTCATGCTAT 283
                                                                                                                                                                                                                                                                                                                                                                      82 AlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnPro 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 AsnAlaArgThrGluValAlaGlnLySIleValArgHisSerLeuLysProCysMetLeu 121
                                              -----SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSer 38
                                                                                         39 LeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrp 58
                                                                                                                                                                                   59 LysIle-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer--- 74
                                                                                                                                                                                                                                                                     -----GluThrAlaCysdlyCysVal
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                                                                      WHE1709_C12_E232S Wheat heat stressed spike cDNA library Triticum aestivum cDNA clone WHE1709_C12_E23, mRNA sequence.
BF429171
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105555773
Fax: 5105555818
                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.
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Triticeae; Triticum.

Triticeae; Triticum.

Tobaces 1 to 646)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han

P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Malatrasi,M., Miller,R.,

Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wheat genomes - Heat stressed spike cDNA library

Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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GGGCTTCTTCCAACCATCTCAGCA 610
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Best Local Similarity:
Query Match:
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Alignment Scores:

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/tissue_type="developing seeds"
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/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
Site_1: Not1; Site_2: Mlu1; mRNA obtained from wheat seeds
of cultivar Gleniea 15 days post-anthesis"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum.
1 (bases 1 to 754)
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Uppublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-02440
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >1.4 kb plate: 030 row: B column: 01
Seq primer: M13 Reverse: Seq primer: M15 Re
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
, Triticeae; Triticum.
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TaE15030B01R TaE15 Triticum aestivum cDNA clone TaE15030B01R, mRNA
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390 GTTGAGCCAAGTCTTCCAACAGCCTCAGCAATA-----TCCATCAGGCCA 440
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270 GCTGTGGCAGATCCCCGAGCAGTCGCGTGCCAAGCCATCCACAATGTTGTTCATGCTAT 329
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       Length:
Matches:
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Contact. Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-4604
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >1.4 kb
Plate: 019 row: D column: 12
Seq primer: M13 Reverse.
Spermatophyta; Tridiplantae; Streptophyta; Embryophyta; Spermatophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.

1 (bases 1 to 677)
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/dev_stage="ls days after anthesis"
/lab_host="E. coli DH10B"
/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea days post-anthesis"
101 g 127 t
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36
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Mismatches:
Indels:

    .677
    /organism="Triticum aestivum"

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Matches:
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/db_xref="taxon:4565"
/clone="TaE15019D12R"
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TaE15019D12R TaE15 Triticum aestivum cDNA clone TaE15019D12R, mRNA
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                       195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9 Tel: (204) 983-2340 Fex: (204) 983-4604 Email: scloutier@em.agr.ca
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Matches:
Conservative:
Mismatches:
Indels:
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BQ245845
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Wheat functional genomics - Gleniea developing seeds cDNA libraries Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (2004) 983-2460
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="developing seeds"
/dev_stage="15 days after anthesis"
/lab_host="E. Coli DHIOB"
/note="vector: pcMv-SPORT6.0 (Invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glalea 134 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ246454 ' 731 bp mRNA linear EST 03-MAY-2002
TaE15010E09R TaE15 Triticum aestivum cDNA clone TaE15010E09R, mRNA
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                                                                                                                                                                                                                                                       486 CCAACAGCCTCTGCAACAATA-----TCCATTAGGCCAGGGCTCCTTCCGGCCATC
     --GluThrAlaCysGlyCysValAlaAspLys
                                                      381 GATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAAAGTTGTTCATGCTAT-----
                                                                                                             85 AlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArg
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Matches:
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/db_xref-"taxon:4565"
/clone-"TaE15010E09R"
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BQ246454
BQ246454.1 GI:20442330
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Cloutier, S.
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Query Match:
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537 TCAGCA 542
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BQ246454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wheat functional genomics - Glenlea developing seeds cDNA libraries
Wheat functional genomics - Glenlea developing seeds cDNA libraries
Uppublished (2002)
Contact: Dr. Sylvia Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
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Fax: (204) 983-4604
Fax: (204) 983-4604
Fax: (204) 983-4604
Fax: (204) 983-600
Fax: (204) 983-800
Fax: (204)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 694
/organism="Triticum aestivum"
/cultiva="Glenlea"
/db_xref="taxon:4565"
/clone="TaEl5008E10R"
/clone="TaEl5008E10R"
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/dev_stage="15 days after anthesis"
/lab_host="E. coli DH10B"
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/note="Vector: pcMv-SPORT6.0 (Invitrogen Technologies);
/site_l: Not!; Site_2: Mlut; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"
32 a 227 c 100 g 135 t
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum.
                                                                                                                                 BQ246558 13-MAY-2002 694 bp mRNA linear EST 03-MAY-2002 Tab15008E10R Tab15 Triticum aestivum cDNA clone Tab15008E10R, mRNA
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BQ246558.1 GI:20442434
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TITLE
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fertilizer, Environment 2) 240C/170C day/night, well-watered, without post-anthesis fertilizer, Environment 3) 370C/170C day/night, well-watered, with post-anthesis fertilizer, Environment 4) 370C/170C day/night, well-watered, without post-anthesis fertilizer, Environment 5) 370C/170C day/night plus drought, with post-anthesis fertilizer, Environment 6) 370C/170C day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and cotal RNA was prepared by S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A CDNA library was made using poly (A) RNA, and the cDNA library was made using poly (A) RNA, and the cDNA library was made using poly (A) RNA, and the cDNA library was made using poly (A) RNA, and the cDNA library was made using poly (A) RNA, and the cDNA library was made using poly (A) RNA, and the cDNA library was made using poly (A) RNA, and the CDNA library was made using poly (A) RNA, and the CDNA library was made using poly (A) RNA, and the CDNA library was adequencing were performed in the OD Anderson lab (others)." BASE COUNT 266 a 257 c 123 g 146 t	Alignment Scores: Pred. No.: Pred. No.: 88 50 Matches: Score: Percent Similarity: 37.848 Conservative: 20 Best Local Similarity: 24.328 Query Match: 13.098 Indels: 41 Os.: 14.	y validation between the problem of	Qy 61	Qy 99 IleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysPro 118 ::: :::
Oy 22 SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLys 41 :::	bb 639 TCAGCA 644 RESULT 22 BQ839009 LOCUS BOR39009 BOR39009 BORSIVum CDNA 1100 WHE3590_C09_F182S Wheat developing grains cDNA 1100 Triticum aestivum cDNA 1000 WESTVUM CDNA 1000 WESTVUM CDNA 1000 WESTVUM CDNA 1000 WESTVUM CDNA 1000 Triticum aestivum CDNA 1100 WESTVUM CDNA 1000 Triticum ACCESSION WERSION BOR39009 GI:22143331 KEYWORDS SOUNCE BOR39009 LOCUS FINANCE FINA	NISM NCE ORS		Apropriate Appropriate Appropriate Appropriate Appropriate Appropriate Appropriate B6" / Cultivar="Butte B6"

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SM Triticum aestivum
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida: Poales; Poaceae; Pooldeae; Triticae; Manipee; Ma, Canada R3T 2M9
Tel: (204) 983-2440
Email: scloutiereem.agr.ca
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/dev_stage="25 days after anthesis"
/lab_host="E. coli DH10B"
/note="vector: pcwv-SPORT6.0 (invitrogen Technologies);
Site_1: Noti; Site_2: Mlu1; mRNA obtained from wheat seeds of cultivar Glenlea 25 days post-anthesis"

229 c 109 g 138 t
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TaE25029B04R TaE25 Triticum aestivum CDNA clone TaE25029B04R, MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >870 bp Plate: 0.29 row: B column: 04 Seq primer: M13 Reverse.
                                                                                                                                                                                           363 -----TATTCTGCATCAACAACAACAACAACAACAACAACCATCGAGCCAGGTCTCCTT 416
         252 AGTTTTGCAACAAAGTACTTACCAGCTGTTACAAGAATTGTGTTTTCAGCACCTATGGCA 311
                                                                                                                                              85 AlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArg 104
                                                                                                                                                                                                                                                                  417 CCAACAGCCTCTGCAACAATA-----TCCATTAGGCCAGGCTCCTTCCGGCCATC 467
                                                        GluThrAlaCysGlyCysValAlaAspLys
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                                                                                              312 GATCCCTGAGCAGTCGCAGTGCCAGCCATCCACAATGTTGTTCATGCTAT------
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Mismatches:

    708
    /organism="Triticum aestivum"

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/db_xref="taxon:4565"
/clone="TaE25029B04R"
/clone_llb="TaE25"
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BQ251408.1 GI:20447284
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BQ251408
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/cultivar="Chinese Spring"
/duref="taxon:4565"
/duref="taxon:4565"
/clone="wheat 20-45 DAP spike cDNA library"
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/tissue_type="spike and seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="vector: Lambda Uni ZAP XR, excised phagemid;
slte_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP
were harvested, total RNA and poly(A) RNA were prepared,
cond library was maded, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
(Choi, Close, Fenton) at the University of California,
Riverside. Plasmid DNA preparations and DNA sequencing
were performed in the OD Anderson lab (all other authors
                                                                                                             Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
; Triticeae; Triticum.
l (bases 1 to 607)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Haia,C.C., Kańg,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
The structure and function of the expressed portion of the wheat
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                         US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tatl: 5105595773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
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aestivum cDNA clone WHE0874_G03_N06, mRNA sequence.
BG262346
BG262346.1 GI:12863468
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BASE COUNT 106 a 257 ORIGIN	Pred. No.: 3.95 Pred. No.: 88.00 Score: 88.00 Percent Similarity: 40.00 Best Local Similarity: 20.80 Query Match: 13.02 DB: 13.02	US-10-048-196-2 (1-134) x BM6 OY 8 ThralaThrLeuMerThra Db 196 ACCGGTTGGGCAGGGGGGGGGGGGGGGGGGGGGGGGGGG	256 48	289 68 337	Oy 88 AlaValSerbeuThrGluL Db 397 CGGTGCAGCTGTTGCGCGT OY 103 AlaargThrGluValAlaG Db 457 CGACGGGTGCGGGGTGCGC	123 Th 517 CT T 26 664	LOCUS BQ838664 DEFINITION WHE3591_C06_E11ZS aestivum cDNA cloo ACCESSION BQ838664.1 GI:22 KEYMORDS EST. SOURCE Dread wheat. ORGANISM Triticum aestivum BURATYOCTA; VITIGIA	REFERENCE 1 (bases 1 to 80 AUTHORS Altenbach,S., And K., Crossman,C., And Milson,C. and Woo TITLE The structure and genomes - Develop JOURNAL Unpublished (2002	US Department Or. West Arca, Wester. 800 Buchanan Stree 800 Buchanan Stree 801 Stores Street 801 Sequences have be 901 Sequences have be 901 Sequences Sequence. Seq primer: SK pr FEATURES Location 808
Db 177 GTATTCGCAACAACAACAATTTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAACA 236	Oy 22SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu 39 :::	Qy 60 Ile74	83 AsplysalaproglualavalSerLeuThrGluLeuThrThrAlaalalleAsnbroAsn 10 11 1 1 1 1 1 1 1 1 1	103 AlaargThrGluv 504 CTCCTTGCAACAC 123 ThrValasnala	RESULT 25 BM634463 DCCATCTCAGCA 500 T14 bp mRNA linear EST 26-FEB-2002 DCCUS DEFINITION 17000687509132 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone	GI: laria gambi Meta Endor	Anopheles. REFERENCE 1 (bases 1 to 714) AUTHORS HOLL,R.A., Lin,JJ., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab AUTHORS ,R., Collins,F.H., Venter,J.C. and Hoffman,S.L. TITLE Celera Anopheles gambiae EST project JOURNAL Unpublished (2002) COMMENT Celera Genomics 45 w. Gude Dr., Rockville, MD 20850, USA Tel: 2404533151 Fax: 2404534580	rimer	/db_kxer="1960044653777" /clone="1960044653777" /clone=lib="A.Gam.ad.cDNA1" /dev_stage="Adult" /lab_host="DH10b" /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3' . Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

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nderson
Agriculture, Agriculture Research Service, Pacific
Trn Regional Research Center
eet, Albany, CA 94710, USA
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liplantae; Streptophyta; Embryophyta; Tracheophyta;
lagnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
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, Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J.,
,O.J. dinction of the expressed portion of the wheat
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TGTTCATCTGCACCAAGCAGGTGTGCCGGCGGACGCGCAAAC 456
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been trimmed to remove vector sequence and low
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/clone_lib="10.2". Ogihara unpublished cDNA library, Wh_e"
/tissue_type="seed DPA10"
/dev_stage="Feekes' scale 11.2"
/dev_stage="Feekes' scale 11.2"
/note="Vector: Lambda Uni-2AP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled from the two
samples, polyA was purified from the TJ Close lab
library was made, and the CDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
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Ogihara,Y. and Murai,K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                     BJ237941 Y. Ogihara unpublished cDNA library, Wh_e Triticum aestivum cDNA clone whello22 3', mRNA sequence.
99 IleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysPro 118
                                      7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAla-----Ser 22
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db xref="taxon:4565"
/clone="whello22"
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                                                                                                                          111 ::: |||||||
179 TTTGCAAGAAAGTACTTACCAGCTGGTGCAACAATTGTGTTGTCA------GCA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 -----CAGGGATGTTGTATTGCAACAACAACATAGCGCATGGAAGCTCACAAGT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 ACAACAACAACAAATCCTACAACAAATTTTGCAACAACAACTGATTCCATG----- 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 GCTGTGGCAGATCCCCGAGCAGTCGCGGTGCCAAGCCATCCACAATGTTGTTCATGCTAT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHis 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------SlaAlaMetLysLeuSerGluSerLysAla 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 -----ValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 GTATTCGCAACCACAACAACTTTCGCAGCAGCAGCAGCAGCAGCAGCAGCAACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 LysIleSerGlu-----ThrAlaCysGlyCys---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 AlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIle----
                             /cultivar="Butte 86"
/db_xref_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_taxon.ci-f_tax
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36
20
51
41
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Matches:
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37.84%
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12.948
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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DB:
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Percent Similarity: 36.81% Conservative: 17 Best Local Similarity: 25.00% Mismatches: 53 Query Match: 12.87% Indeb: 38 Best Local Similarity: 25.00% Mismatches: 53 Query Match: 12.87% Gaps: 6 US-10-048-196-2 (1-134) x BE423599 (1-536) Qy 7 ValThralaThrLeumetThralaPheThrLeualaSerCysala	259	Db 418TATTCTGCATCAACAAAACAACAACAACAACAACAACCAGGT 465 Qy 103 AlaArgThrGluValalaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122 ::: Db 466 CTCCTTCCAACAGCTCTGCAACAATATCCATTAGGCCAGGGTCCTTCCG 516 Qy 123 ThrValAsnAla 126 ::::: Db 517 GCCATCTCAGCA 528	RESULT 29 BQ246932 LOCUS BQ246932 LOCUS DEFINITION TaE15003D12R TaE15 Triticum aestivum cDNA clone TaE15003D12R, mRNA ACCESSION BQ246932.1 GI:20442808 KEYWORDS EST. ORGANISM Triticum aestivum CNGANISM Triticum aestivum Spermatophyta; Embryophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poaceae; Pooldeae : Triticaee; Triticum. Ammunos I (bases 1 to 610)	· • • • • • • • • • • • • • • • • • • •
43 AlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAla 43 AlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAla 43 AlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAla 574CAGGGATGTTGTATTGCAACACACACATAGGCATAGGAAGTTCACAAGT 62AlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCys 1	12 TCTGCATCAACAACAACAACAACAACAACCAACCTTGAGCCAGGTCTGCTTGAGCAGGTCTGCTTGAGCAGGTCTGAGCAGGTCTGAGCAGGTCTGAGCAGGTCTGTGTGAGACAACAACAACAATAATGCATCAGGCCAGGGCTCCTTCCAGCCATGGAGAGAACAATATCCATCAGGCCAGGGCTCCTTCCAGCCATGGAGAGAGAATATGCATCAGGCCAGGGCTCCTTCCAGCCATGGAGAGAGAATATGCATCAGGCCAGGGCTCCTTCCAGCCATGGAGAGAGAATATGCATCAGGCCAGGGCTCCTTCCAGCCATGGAGAGAGAGAATATGAGAGAGA	VERSION BE423599.1 GI:9421442 KEYWORDS EST. SOURCE bread wheat. ORGANISM Triticum aestivum Spermatophyta; Viridiphantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum. REFERENCE 1 (bases 1 to 536) AUTHORS Altenbach, S., Anderson, O.D., Chao, S., Galili, G., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.	TITLE The structure and function of the expressed portion of the wheat genomes - Endosperm cDNA library JOURNAL Unpublished (2000) COMMENT Contact: Olin Anderson US Department of Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA 7e1: 5105595818 Fax: 5105595818 Email: oandersn@pw.usda.gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer. FEATURES Location/Qualifiers Source	/org/ /cul- /clc /clc /clc /clc /lat /not /not /not /not /not /not /not /no

reverse

```
//Ugantam="filticum" descivum
//Cultivam="filticum" descivum
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Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenhea 15 days post-anthesis"
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BRY_11500 BRY Triticum aestivum cDNA clone P52-1L, mRNA sequence.
AW448815.1 GI:12019350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 ACAACAACAACAACAACAAGAACAACAATTCCTTCAACAAATTTTGCAACAACAACTGAC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101. ProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMet 120
                                        sequences generated with rewith forward primer and 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 TCCATG------CATGGATGTTGTATTGCAGCAACAACATAGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     631
38
17
51
51
                Email: scloutier@em.agr.ca
was cloned directionally, not all sequenc
primer were from the 5' end (same with fo
Average insert size 1s >1.4 kb
plate: 032 row: G column: 05
Seq primer: M13 Reverse.
Location/Qualifiers
1. 631
/organism="friticum aestivum"
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Indels:
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Matches:
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87.00
37.67
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bread wheat.
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Query Match:
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ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
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AW448815
                                                                                                                                    FEATURES
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/note="vector: pCMV-SPORT6.0 (Invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"
a 2011 190 g 116 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wheat functional genomics - Glenlea developing seeds cDNA libraries Wheat functional genomics - Glenlea developing seeds cDNA libraries Contact: Dr. Sylvie Cloutier Cereal Research Cente, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9 Tel: (204) 983-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ244975 13-MAY-2002
Tabl5032G05R Tabl5 Triticum aestivum cDNA clone Tabl5032G05R, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499 CTCCTTCCAACAGCCTCTGCAACAATA-----TCCATTAGGCCAGGGCTCCTTCC 549
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232 ACAACAACAACAACAACAAACATTCAACAATTTTGCAACAACAACTGATTCCATG 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 Ile-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GluThrAlaCysGlyCysValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 ATGGCAGATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAATGTTGTTCATGCTAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 -----SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu
                                                                                                                                                                                                                                                                                                                                                                                 7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAla----
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Conservative:
Mismatches:
Indels:
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/clone_lib="TaE15"
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BQ244975.1 GI:20440851
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                                          soybean.
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                 Streptophyta; Embryophyta; Tracheophyta;
ta; Lillopsida; Poales; Poaceae; Pooideae
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167 ACAACAACAACAACAAGAACAACAAAAATTCTACAAAATTTTGCAACAACAACTGAC 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMet 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 CCAGGTCTCCTTCCAACAGCCTCAGCAACAATA-----TCCATTAGGCCAGGGCTC 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrPro---
                                                   Clarke, B.C., Hobbs, M. and Appels, R. Genes active in developing wheat endosperm unpublished (2000)
Contact: Bryan Clarke
Division of Plant Industry
C.S.I.R.O.
GPO Box 1600, Canberra, ACT, Australia
Tel: 61 2 6246 5054
Fax: 61 2 6246 5000
Email: bryanc@pi.csiro.au.
                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                   /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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202 c 101 q
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              Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
; Triticeae; Triticum.
Triticum aestivum
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                /cultivar="Wyuna
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26.03%
12.87%
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/organism="Glycine max"
/db_xref="taxon:3847"
/clone_"Gm-r1083-2285
/clone_"Gm-r1083-2285
/clone_"Ib-"Gm-r1083-2285
/clone_"Ib-"Gm-r1083-2285
/clone_"The library Gm-r1083 is a sequence-driven, reracked set of 4,992 clones selected from cDNA libraries from various tissues and stages from the progenitor library Gm-clo09 (from mature roots of 2 month old greenhouse grown 'Williams' soybeen plants); 820 sequences from the progenitor library Gm-cl003 (from Supernod') (from 2 to 3 week old whole plants of Williams); and 3055 sequences from library Gm-cl028 (from Supernod') plants whose seedlings were innoculated with Bradyrhizobium japonicum, courtesy of Dr. Gary Stacey). The S' ESTs. of the source clones from the different progenitor libraries was used to select singletons, or a representative of each contig, which were reracked com-r1083 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://web ahc umn.edu/blodata/nsfspy/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available through: Incyte Genomics, 4633 World Parkway (Irrcle St. Louis, Missouri 63134. Phone (800) 430-0030 or (314) 427-3222 FAX: (314) 427-3324. Web site: http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reracking was performed by Incyte Genomics, St. Louis, http://www.incyte.com, and 3' sequencing by the Keck Center for Comparative and Punctional Genomics, University of Illinois, http://www.lie.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1083 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Incyte Genomics clone ID of the original cDNA library that is also listed under 'OTHER EST'."
                                                                                                                                                                                                                                                                                                                  J. (bases, L.O. 941).
Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., Erpelding, J., Reph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
Other_ESTs: AW203461 corresponding to Gm-c1028-1497 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional
                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: 5'-TTTTTTTTTTTTTTTT(A/C/G)-3'.
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Mismatches:
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1. .641
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GI:16343286
                                                                                                                                                                                                                                                                                                   (bases 1 to 641)
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87.00
40.88%
29.20%
                                                                                                            Glycine max
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Query Match: DB:	ch: 12.87% Indels: 26 . 13 Gaps: 8	Score: Percent Similarity:
US-10-048-196-2	-196-2 (1-134) x BI968881 (1-641)	Best Local Similarity: Query Match:
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Db 130	ATAGCATACAATCTGT	- TO-048-
Oy 24	ProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla 43 ::: ::: CGGAAGAAAGTTGAAGGGGAAGAAGGGGGAAGAAGGGGGAAGAA	Oy 7 VALThrAlaThrLe 11 11 Db 107 GTATTCGCAACCAC
		Δλ 25
Oy 44 Db 244	ValtysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIlealaalaMet, 63 	-
		Qy 38 SerLeuIleLysHi
Uy 64	LysbebserserstuserLysalaryslleserGluThrAlaCysGlyCys 80 	Db 227 TCCATG
81	ValAlaAspLysAlaProGluAlaValSerLeuThrGluLeu	Qy 58 TrpLysile
m	AGCACGCGGGGTTCTCCAGCTTAACAGTGCCTGAATCCTCTCTCT	TGGA
Qy 95	ThrThralaalalleAsnProAsnAlaargThrGluValAlaGlnLysIleValArgHis 114	75
Db 394		329
0y 115	SerLeuLysProCysMetLeuGluThrValAsnAlaPheIle 128	Qy 81 ValAlaAspLysAl
	 TCTCACTAGGT	Db 389 TAT
RESULT 33		Oy 101 ProAsnAlaArgTh
BQ605913		Db 434 ccAGGTCTCCTTCC
DEFINITION		Qy 121 LeuGlurhrvalAs
ACCESSION VERSION	BQ605913 BQ605913.1 GI:21555048	Db 485 CTTCCGCCATCTC
KEYWORDS SOURCE		r 34 877
ORGANISM	Triticum aestivum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache	LOCUS BQ251877 DEFINITION TAE25023A08R
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.	NO
REFERENCE		
TITLE	Assessing the utility of Arabidopsis genomic information for interpreting wheat EST sequences	×
JOURNAL		
	, A	TITE Whost functi
	Fax: 1 650 325 3748	AL
FEATURES	Email: Inee	Conment Contact: Dr.
sonrce		195 Dafoe Rd Tel: (204) 9
	/cultivar="Wyuna" /db_xref="taxon:4565"	Fax: (204) 9 Email: sclou
	/clone_lib="wheat EST endosperm library" /tissue_type="endosperm"	was cloned d
	/dev_stage="developing endosperm tissue θ, 10 and 12 DPA (days post anthesis)"	Average inse
BASE COUNT ORIGIN	215 a	Seq primer: FEATURES Loc source 1.
Alignment Scores: Pred: No.:	Scores: 4.32 Length: 641	/or
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Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
yta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
e; Triticum.
1 to 643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 bp mRNA linear EST 03-MAY-2002 BR TaE25 Triticum aestivum cDNA clone TaE25023A08R, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tional genomics - Glenlea developing seeds cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outler@em.agr.ca
directionally, not all sequences generated with reverse
e from the 5' end (same with forward primer and 3' end).
Sert size is >870 bp
row: A column: 08
: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                            hrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMet 120
                                                                                                                                                                  NaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SATCCCTGAGAAGTTGCAGTGCCAGGCCATCCACAATGTTGTTCATGC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------GluSerAsnProLysAsnSerSerAlaAsnLeuThrThr 37
                                                                                                                                                                                                                                                                                                                                                                                                                               -----GluThrAla-----CysGlyCys 80
                                                                                                                                             euMetThrAlaPheThrLeuAlaSerCysAlaSerThrPro----- 24
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Tr. Sylvie Cloutier
earch Centre, Agriculture and Agri-food Canada
Rd, Winhpeg, MB, Canada R3T 2M9
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                                                                                                            x BQ605913 (1-641)
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Best Local Similarity:
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                         /tissue_type="developing seeds"
/dev_stage="25 days after anthesis"
/dev_stage="25 days after anthesis"
/nab_host="E. coli DH10B"
/note="vector: pcWv-SPORT6.0 (invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 25 days post-anthesis"
a 204 c 106 g 127 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ246079 647 bp mRNA linear EST 03-MAY-2002 TaE15016E10R TaE15 Triticum aestivum cDNA clone TaE15016E10R, mRNA sequence.
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Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 647)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                                                                                                                                                                                                                                   ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAla-----
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36
117
53
38
                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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87.00
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BQ246079.1
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Best Local Similarity:
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LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                BASE COUNT
                                                                                                                                                                        Pred. No.:
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AUTHORS
TITLE
JOURNAL
COMMENT
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/organism="Triticum aestivum"
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/cultivar="Glenlea"
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Site_1: Not!: Site_2: Mlu!; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"
/ra 197 c 105 g 128 t
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TaEl5 Triticum aestivum CDNA clone TaEl5039G10R, mRNA
                                                                         with reverse and 3' end).
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                                                                         sequences generated
with forward primer
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117
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38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
Tel: (204) 983-2340
Eax: (204) 983-4604
Email: scloutier@em.agr.ca
was cloned directionally, not all se
primer were from the 5' end (same with a separage insert size is >1.4 kb
Plate: 016 row: E column: 10
Seq primer: M13 Reverse.
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Matches:
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VERSION
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Spermatophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases 1 to 652)
Cloutier, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="developing seeds"
/dev_stage="25 days after anthesis"
/lab_host="E. coli DH10B"
/note="vector: pcwv-SPORT6.0 (invitrogen Technologies);
Site_1: NotI: Site_2: MluI: mRNA obtained from wheat seeds
of cultivar Glenlea 25 days post-anthesis"
                                                                                                                                                                                                                                                                                                                                                                                             Wheat functional genomics - Glenlea developing seeds CDNA libraries Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Corteal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tal: (204) 983-2440
Fax: (204) 983-4604
Fax: (204) 983-66m.agr.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Plate: 011 row: E column: 12
Seq primer: All Reverse.
                                                                                                                                                     BQ249968 652 bp mRNA linear EST 03-MAY-2002
TaE25011E12R TaE25 Triticum aestivum cDNA clone TaE25011E12R, mRNA
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Mismatches:
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Matches:
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87.00
37.67
26.03
12.87
                                        123 ThrValAsnAla 126
                                                                  488 GCCATCTCAGCA 499
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BQ249968.1
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Best Local Similarity:
Query Match:
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                                                                                                                                            Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Coreal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipey, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-604
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >1.4 kb
Plate: 039 row: G column: 10
Seq primer: M13 Reverse.
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/dev_stage="15 days after anthesis"
/lab_host="E. coli DH10B"
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Site_1: NotI; Site_2: MluT; mRNA obtained from wheat seeds of cultivar Glenlea 15 days post-anthesis"
207 c 106 g 128 t
                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticoae; Triticom.
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Indels:
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87.00
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25.00%
                                        riticum aestivum
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Query Match:
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7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrPro----
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-24604
Email: scloutier@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="developing seeds"
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a 195 c 104 g 136 t
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
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                                                                                                  81 ValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
                                                                                                                               398 TAT------TATTCTGCATCAACAAAAAACAACAACAACAACAACTATCGAG 442
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/tissue_type="developing seeds"
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Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"
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SerLeulleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyr
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Contact: Dr. Sylvie Coutier
Cereal Research Centre, Agriculture and Agri-food (195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Fax: (204) 983-2340
Email: scloutier@em.agr.ca

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/organism="Triticum aestivum"

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FEATURES Location/Qualifier 1674 /organism="Triticu /cultivar="GlenLea /db_xref="taxon:45 /clone="Tax2500580 /clone="Tax2500580 /clone="Tax2500580 /clone="Tax2500580 /clone="Tax25" /tissue="type="deve" /dev_stage="E. coli /lab_host="E. coli /clone="type="tax25" /lab_host="E. coli /clone="type="tax25" /clone="type="tax25" /clone="tax25" /clone=	SILE_INCLIS SILE Of Cultivar Glenle BASE COUNT 236 a 214 c 100 g ORIGIN	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Percent Similarity: Best Local Similarity: Duery Match: DB: US-10-048-196-2 (1-134) x BQ250428 (1-6	Qy 7 ValThralaThrLeuMetThralaPheTh	Qy 38 SerLeulleLysHisAlaValLysGlnTh : : : : : Db 326 TCCATG	81 488 101 101 533 121 584	Search completed: May 5, 2003, 23:15:5 Job time: 1069 secs
BASE COUNT 227 a 210 c 99 g 122 t ORIGIN Alignment Scores: 4.52 Length: 658 Pred. No.: 87.00 Matches: 38 Score: 87.00 Matches: 17 Percent Similarity: 26.03% Mismatches: 17 Best Local Similarity: 26.03% Mismatches: 51 Query Match: 12.87% Indels: 40 DB: 14.05 7	7 ValThralaThrLeuMetThralaPheThrLeuAlaSerCysAlaSerThrPro	OB 159 GTATTCGCAACCAACAACCAATTTCACAGCAGCAGCAGCAGCAACAACAACAACA 218 QY 25	ACAAGTTT GCAGATCC LysAlaPr	441 TATTATTCTGCATCAACAACAACAACAACAACAACTATCGGG 101 ProAsnalaargThrGluValalaGlnLysIleValArgHisSerLeuLysProCysMet	RESULT 40 BQ250428 BQ250428 LOCUS LOCUS LOCUS BQ250428 BQ250428 Triticum aestivum cDNA clone TaE25005B09R, mRNA ACCESSION BQ250428 BQ250428 BQ250428 Triticum aestivum BQ250428 Triticum aestivum BQ250428 Triticum aestivum SGURCE CNGANISM Triticum aestivum SPERENCE Triticum aestivum Triticum aestivum SPERENCE Triticum aestivum	AUTHORS Cloutier,S. TITLE Wheat functional genomics - Glenlea developing seeds CDNA libraries JOURNAL Unpublished (2002) COMMENT Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9 Tel: (204) 983-4604 Email: scloutier@em.agr.ca was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >870 bp Plate: 005 row: B column: 09 Seq primer: M13 Reverse.

veloping seeds"
ays after anthesis"
11 DH10B"
CMV-SPORT6.0 (invitrogen Technologies);
te_2: Mlul; mRNA obtained from wheat seeds
lea 25 days post-anthesis" ThrLeualaSerCysAlaSerThrPro---- 24 NanProLysAsnSerSerAlaAsnLeuThrThr 37 ||||||| :: |||| |ATCCTTCAACAATTTTGCAACAACAACTGAC 325 erLeuThrGluLeuThrThrAlaAlaIleAsn 100 la-----CysGlyCys 80 hrCysGlnThrGlnLeuThrGlyHisGlnTyr 57 ysLeuSerSerGluSerLysAlaLysIleSer 74 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: cum aestivum" ea" 4565" 809R" 674)

SUMMARIES

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Command line parameters:
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-NO_XLPXY -NO_MMAP -LARGEQFRY -NCE_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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		Moraxell	Ø	catarrhal	1.S	train	ATCC43617 BASI	•
		BASB125		protein;	protein; strain	ATCC	ant	ccine;
		genetic hearing		unisat	ion; fnes	fect	infection; upper respiratory tracts; pneumonia; sinusitis; nosocomial	ract; otitis media; mial infection;
	X X	invasiv	e di	disease;	ant	cter	uditory; ds.	
		Moraxella		catarrhali	halis.			
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The invention relates to the Moraxella catarrhalis strain ATCC43617

BASB125 protein (AAB60646) and to DNA encoding it (AAF59800). The
Invention also relates to immunogenic fragments of the BASB125 protein,
expression vectors and host cells comprising BASB125 nucleic acids, the
recombinant production of BASB125, vaccine compositions comprising the
BASB125 protein or incleic acid, an antibody against BASB125, therapeutic
compositions comprising the anti-BASB125 antibody, and a method of
identifying a Moraxella catarrhalis infection via the detection of
BASB125 proteins or antibodies. The vaccine compositions of the invention
are useful as prophylactic or therapeutic agents against Moraxella
catarrhalis infections in mammals, particularly humans. Moraxella
catarrhalis is a Gram negative bacterium frequently isolated from the
human upper respiratory tract, which is responsible for several
pathological conditions. It is responsible for about 15% of otitis media
cases in children (which can lead to temporary or permanent hearing
loss). It also causes pneumonia in elderly people, and sinusitis,
cosocomial infections and, less frequently, invasive diseases. BASB125
proteins or nucleotides may additionally be used in screening for novel
antibacterial compounds, and in the diagnosis and staging of infections. The present sequence represents DNA encoding the Moraxella catarrhalis
the present sequence represents DNA encoding the Moraxella catarrhalis
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                                                                                                                                                                                                                                                        New BASB125 polypeptide isolated from Moraxella catarrhalis for treating, preventing and diagnosing diseases associated with M. catarrhalis infection in mammals, e.g. otitis media in humans
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P-PSDB; AAB60646.
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The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otticis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                             Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
               ProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysffroCysMet 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
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01-MAY-1998;
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                                                                                                                                                                                                                                             Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
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Scarselli
                                                 ProAsnalaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMet
                                                                                                                                                                                                                                 Neisseria meningitidis ORF 108 partial DNA sequence SEQ ID NO:385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
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Scalato E,
                                                                                                                                                 LeuGluThrValAsnAlaPheIleValProThrThrArg 134
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Ratti
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Rappuoli
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98US - 0094869.
98US - 0099894.
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Tettelin H, Venter JC;
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, Pizza M,
                                                                                                                                                                                                                                                                             Neisseria meningitidis
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P-PSDB; AAY74455.
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polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseriab bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGCCGGGGGCGGTAACACTTCGGCAGCTTAGACGCGGCGCACAGGTATGGGCGGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrp
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                                                                                                                                                                                                                                                                             Sequence 522 BP; 134 A; 143 C; 147 G; 98 T; 0 other;
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Conservative:
Mismatches:
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118.00
47.118
23.148
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                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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119 Cys 119

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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ5457 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polyneptides, antibodies and compositions of the Invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
                                                                                                                                                                                        Masignani V, Mora M;
Scalato E, Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                            to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                        Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                        Hickey E,
Ratti G,
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                                                                                                                                                                                   Galeotti C, Grandi G, H
, Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 319; 1453pp; English.
                                                 98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
98US-0094869.
98US-0098994.
98US-0099062.
                                                                                                                                     (CHIR ) CHIRON CORP.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                     Petersen J, Pizza M,
Tettelin H, Venter JC;
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                                                   09-0CT-1998;
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25-FEB-1999;
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Sequence 522 BP; 129 A; 142 C; 152 G; 99 T; 0 other;

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151 ATGAATAAAACCTTGTCTATT-----TTGCCGGTGGCAATCTTACTCGGCGGCTGC 201
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                                                                                                                                                         1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
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29
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59
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             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                            Gaps:
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                0.000495
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46.28%
23.97%
17.16%
                                            Percent Similarity:
Best Local Similarity:
Alignment Scores:
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DB:
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CIGGCICCGICCACGCGCAAICAGGCACITGCCGCCTGACGCCAAAACGGITICCGCC 498

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represent specifically claimed Nelseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB2563 represent Nelseria DNA sequences and their corresponding proteins; AAA81264 to Nelseria DNA ASA81264 to AAA81259 and AAA81264 to Expension of Nelseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Nelseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Nelseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used as a medicament (or in the manufacture of a composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Maningococcus B; against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Maningococcus B vaccines have failed mainly due to antigen tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scarlato V;
                                                                                                                                                                                                                                                   Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tettelin H, Venter JC;
Ratti G, Scarselli M,
                                                                                                                                                                                                              N. meningitidis partial DNA sequence gnm_12 SEQ ID NO:12.
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C, Mora M,
                                                               AAA81464/c
ID AAA81464 standard; DNA; 102634 BP.
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99US-0132068
                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis.
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Rappuoli R, Pizza M;
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30-APR-1999;
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499 TGC 501
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CTGGCTCCGTCCACGCGCAATCAGGCACTTGCCGCCTGACGCCCAAAACGGTTTCCGCC 60138
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                                                                                                                                                                                  GCCGCCGGAGGCGGTAACACATTCGGCAGCTTAGACGGTGGCACAGGCATGGGCGGCAGC 60375
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Rappuoli R;
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                                                                                                                                                                                                                                                              LysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCys 78
                                                                                                      {\tt MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys}
                                                                                                                                                                                                            LeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrp
                                                                                                                                                                                                                                                                                                                  GlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla
                                                                                                                                                         AlaSerThrProGluSer----AsnProLysAsnSerSerAlaAsnLeuThrThrSer
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Scarlato V,
    23
27
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 Matches:
Conservative:
Mismatches:
Indels:
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Galeotti C, Mora M, Ratti G, Scarselli M, S
Frazer CM, Grandi G;
                                                                             US-10-048-196-2 (1-134) x AAA81464 (1-102634)
                                                      Gaps:
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ID AAF21609 standard; DNA; 349980 BP.
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08-OCT-1999; 99WO-US23573.
28-FEB-2000; 2000GB-0004695.
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            Percent Similarity:
Best Local Similarity:
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                                        Query Match:
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Neisseria meningitudis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF215607 are repeated at the beginning of AAF21608, and so on of AAF21545 to AAF21588 encode the Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to the present invention. The NMB genome and fragments from it have attribacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which bluds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial
                                                                                                                                                                                                                                                                                                                                                                                                                                  bacteria. Computers, computer memory, computer storage médalum or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 163966 GCTTGCGTCGCCAAGAAGGACGGATGACGGCAACGATGTG---ATGCAGATG 163910
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                                                                 present invention describes the full length genome
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                   Claim 7; Appendix A; 692pp; English
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ID AAA81490 standard; DNA; 1437668 BP.
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 capresent specifically claimed Neisseria meningitidis genomic DNA sequences tapefilically claimed Neisseria meningitidis proteins; AAA81264 to AAA81303 and AAB25620 to AAB2563 represent Neisseria DNA sequences; and AAA81324 to AAA81325 and AAA81324 to AAA81321 represent PCF primers used in the constant of Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF composition or he used in the manufacture of a composition or he used in the manufacture of a composition or he used in the manufacture of a composition or he used in the manufacture of a composition or he used in the manufacture of a composition of bordensent) for treating, preventing or diagnosing infection que to Neisserial bacteria. For example, some of the identification of sequences and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes; wentiqued an opportunity the provision of further, complete conserved provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and conserved than and penning the conserved than and penning the conserved than and the conserved than an energy and conserved than and conserved than an energy an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scarlato V;
                                                                          Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                      N. meningitidis B full length genome DNA sequence SEQ ID NO:1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tettelin H, Venter JC;
Ratti G, Scarselli M,
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Masignani V, Galeotti C, Mora M,
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99US-0132068
                                                                                                                                                                                    Neisseria meningitidis
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Rappuoli R, Pizza M;
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Sequence 1437668 BP; 344338 A; 353206 C; 385074 G; 355045 T; 5 other; Conservative: Mismatches: Indels: Length: Matches: 27.7 116.00 46.28% 23.97% 17.16% Percent Similarity: Best Local Similarity: Alignment Scores: Score:

other more variable regions

US-10-048-196-2 (1-134) x AAA81490 (1-1437668)

Query Match:

Gaps:

Db 1064196 ATGAATAAAACCTTGTCTATT-----TTGCCGGTGGCAATCTTACTCGCGCGCTGC 1064146 1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys 20 à

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Db 1063908 CTGGCTCCGTCCACGCGCAATCAGGCACTTGCCGCCCTGACCGCCAAAACGGTTTCCGCC 1063849
                           Db 1064145 GCCGCCGGAGGCGGTAACACATTCGGCAGCTTAGACGGTGGCACAGGCATGGGCGGCAGG
                                                                                                                                        DD 1064025 CGTTTGACCGCCTGCCGATGAGTGCCGAAAAACAGGCGGGAGTGGGAAAACAAGATTGC_1063966
                                                                                       Db 1064085 ATCGTCAAAATGGCGGTTGGGAGCCAATGCCGTGCGGAATTGGACAAACGCAAATGG 1064026
                                                                                                                                                                                                                Db 1063965 GCTTGCGTCGCCCAAGAAGCACCGAACGGATGACCGGCAACGATGTG---ATGCAGATG 1063909
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Scalato E, Scarselli M;
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                                                                                                                                                                                                                                                99 IleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysPro 118
21 AlaSerThrProGluSer----AsnProLysAsnSerSerAlaAsnLeuThrThrSer 38
                                                            39 LeulleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrp 58
                                                                                                                        59 LysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCys 78
                                                                                                                                                                                  79 GlyCysValAlaAspLysAlaProĠluAlaValSerLeuThrGluLeuThrThrAlaAla 98
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Ratti
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Rappuoli R,
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98US-0098994.
98US-0099062.
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Tettelin H, Venter JC;
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P-PSDB; AAY74453.
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02-SEP-1998;
02-SEP-1998;
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and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, and compositions of immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Nelsserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Nelsseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polypurcleotides of the invention may also be used in gene therapy protocols.
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TGCGCTACCGAAGAAGCACCTAACCAGCTGACGGCAACGATGTG---ATGCAGATGCTG 438
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262 GTCAAAATGACGGTAGAAAGCCAATGCCGTGCGGAATTGGACAGGCGCAGCGAATGGCGT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 GCCGCCGGCGAACACATTCGGCAGCTTAGACGGCGCGCACGGGTATGGGTGGCAGCATC 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae; S. pneumoniae; genome; diagnosis; assay; able medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                      MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAATAAAACCTTGTCTATT-----TTGCCGGCGGCAATCTTACTCGGCGGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaSerThrProGluSer---AsnProLysAsnSerSerAlaAsnLeuThrSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IlealaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae genome fragment SEQ ID NO:28.
                                                                                                                                                                                                                                             519
26
29
60
5
                                                                                                                                                                                               Sequence 519 BP; 133 A; 142 C; 149 G; 95 T; 0 other;
                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                       US-10-048-196-2 (1-134) x AAZ53215 (1-519)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV52161 standard; DNA; 5857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
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110.50
45.83%
21.67%
16.35%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae
                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-1996;
                                                                                                                                                                                                                             Alignment Scores:
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID No:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO:1 to 391. The nucleotide sequence at least 95% identical to SEQ ID NO:1 to 391. AAV52524) are genomic fragments from SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from clocked by neumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the rucleic acid molecules by a process comprising: do:) screening a genomic DNA library using as a process comprising: do:) screening a genomic DNA library using as a process comprising: of the sequences in SEQ ID NO:1 to 391, identifying members of the 1brary which contain sequences that hybridise to the target sequence and isolating ment the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification and isolating the amplified sequences. The computer the amplification and isolating the S. pneumoniae genome to prime the amplification modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and the present invention can be used in diagnosis kits and assays, and the present invention can be used in diagnosis kits and assays, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||| ::: ||||||||||:::
5016 AATGAAAATGATAAACTTACGTCCAAGCAAATTAAAATTCATAGATGCCATGCTTACCGAG 4957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 TrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAla---LysIleSerGluThr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AlaValLysGlnThrCysGln------ThrGlnLeuThrGlyHisGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGlu-----Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .836 ACAACTCAAATGCTTTATTAGCATCATCTAACGCTGTTTCTGTACTCAATGATATTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical compositions and vaccines for S. pneumoniae.
    Fannon M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 1800 A; 1173 C; 814 G; 2070 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5857
28
22
38
15
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    Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                              Claim 1; Page 309-312; 1409pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-048-196-2 (1-134) x AAV52161 (1-5857)
Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.9
88.50
48.54
27.18%
13.09%
                        Rosen CA;
    Choi GH,
                                                              WPI; 1998-272225/24.
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5857
  SC,
CA,
                                                                                                                                                                          pneumoniae
  Barash
Kunsch
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RESULT 10 AAN90096

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3312 -----TATTCTGCATCAACAACAACAACAACAACAACCACGAGCCAGGT 3359
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                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                           βÞ
                                                                                                                                           CDNA; 3057
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                                                                                         3411 GCCATCTCAGCA 3422
                                                                            123 ThrValAsnAla 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-367020/38.
                                                                                                                                           AAD08348 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA,
                                                                                                                                                                AAD08348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen
                                                                                                                      RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3255 ATGGCAGATCCCTGAGCAGTCGCAGGCCATCCTCAAAGTTGTTCATGCTAT--- 3311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                  The preferred gene fragment in the patent of the invention encodes alpha-gladin or glutenin, and the preferred plasmid encoding alpha-gliadin is PAY 31. The plasmid may be used for the prodn. of alpha-gliadin, which may be used in the food technology industry to modify prodn. processes of doughs and batters and to reduce unit costs. Gliadin may also be used for diagnosis and treatment of illness caused by wheat gluten proteins and for testing theories of dough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -------CATGGATGTTGTATTGCAGCAACACATAGCGCATGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3195 ATCACAAGTTTTGCAACAAAGTACTTACCAGCTGTTGCAAGAATTGTGTTGTCAACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GluThrAlaCysGlyCysValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 Ile-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer----
                                                                                    Coeliac disease diagnosis; dough formation; food technology; ds.
                                                                                                                                                                                                                                                                               New wheat gluten protein gene plasmid - useful for genetic transformation of yeasts to produce gliadin or glutenin
                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
                                                                                                                                                                                                                                        Litts JC
                                                              Sequence of plasmid pAY31 encoding wheat alpha-gliadin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAla---
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6978 BP; 2042 A; 1631 C; 1447 G; 1858 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                        Anderson OD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
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                                                                                                                                                                                                                                       Neill JD,
                                                                                                                                                                                                                                                                                                               Disclosure; Fig 4; 21pp; English.
  BP
AAN90096 standard; cDNA; 6978
                                                                                                                                                                                                                 (UYHA-) UNIV OF HAWAII (USDA)
                                                                                                                                                                         86US-0922616.
                                                                                                                                                                                            86US-0922616.
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.5
88.00
37.50%
25.00%
113.02%
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                                                                                                                                                                                                                                                           WPI; 1989-150270/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                        24-OCT-1986;
                                                                                                                                                                                            24-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                             US4826765-A
                                          22-MAR-1991
                                                                                                                                                   02-MAY-1989
                                                                                                                                                                                                                                       Greene FC,
                                                                                                                                                                                                                                                                                                                                                                                                              formation.
                     AAN90096;
                                                                                                         Wheat.
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9
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AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted protein genes and AAE03898-AAE03947 represent the proteins they encode. AAE03948-AAE03996 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; has made disease; rhemmatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; Alzheimer's disease; ski disorder; psoriasis; gapsis; diabetes; atheroselerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; anglogenic disorder; kidney disorder; and office disorder; kidney disorder; cendocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein-encoding gene 4 cDNA clone HBMBD51, SEQ ID NO:14.
                                                                                               3360 CICCTICCAACAGCCICIGCAACAATA-----TCCATTAGGCCAGGGCTCCTICCG 3410
103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a //product= "Human secreted protein precursor" //tranal_except= (pos:524..526, aa:Xaa) //note= "Xaa equals any of the naturally occurring L-amino_acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome -
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/product= "Mature human secreted protein"
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treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 50 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoletic disorders, diseases of the immune system, allergies, neurological disorders, eig., Alzheimer's disease, Parkinson's disease, cardiovascular disorders (e.g., rheumatoid arthritis), inflammation, altergies, neurological disorders, eig., Alzheimer's disease, cardiovascular disorders, anglogenic disorders, atherosclerosis, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healthy and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell
                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                            culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.
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Drosophila; developmental biology; cell signalling; insecticide;

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                          23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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84.50
39.06%
24.22%
12.50%
pharmaceutical; gene; ss.
                           Drosophila melanogaster.
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Best Local Similarity:
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3794 CGAATCCACCACCAGTTCCATCACAGACTTGGCCCGACTGGAGAAGATGAAGGTCTCTGA 3735
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     53 ThrGlyHisGln-TyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLy 72
                                                                                                 72 sIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuTh
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22-DEC-2000;
16-FEB-2001;
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                                                                                                                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 10070.
                                                                                                                                                                                                                                                                                                                                            developmental biology; cell signalling; insecticide;
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                                 1602 TGAGAGGCTGAAACCGTATCTG 1623
121 uGluThrValAsnAlaPheIle 128
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ID ABL05196 standard; cDNA; 6959
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                            Drosophila;
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                                                                                                                                                                                                ABL05196;
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BP.

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prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antisense inhibitors of genes essential to
                                            Staphylococcus aureus DNA for cellular proliferation protein #423.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotides for the identification and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibiotics, comprise sequences of antisense nucleic acids
                                                                                        Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; Seg ID No 4588; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                      2000US-206848P.
2000US-207727P.
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2000US-253625P
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(first entry)
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                                                                                                                                                             Staphylococcus aureus
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13 ThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSer

US-10-048-196-2 (1-134) x ABL05196

ð qq

Query Match:

Gaps: (1-6959) AlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeu

33 3872

qq ò

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16-FEB-2001; 2001US-269308P.
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The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Source: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                             MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAla------PheThr 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus DNA for cellular proliferation protein #1284.
                                                                                                                                                                                                                                                                      ---ProGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                      0 other;
                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                     Sequence 921 BP; 322 A; 135 C; 189 G; 275 T;
                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                         (1-921)
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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84.00
45.308
29.068
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                                                                                                                                                                Best Local Similarity:
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                                                                                                                                                      Percent Similarity:
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22-DEC-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella proummoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                 New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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119
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Matches:
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                                                       Zyskind JW,
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84.00
45.30%
29.06%
12.43%
                                                       KĽ,
(ELIT-) ELITRA PHARM INC.
                                                     Ohlsen I
Xu HH;
                                                                                                                                2001-611495/70
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                                                                                                                                                            P-PSDB; AAU37113
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                                                  Haselbeck R,
Yamamoto RT,
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AAV74758/c
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16-MAR-1999

misc_feature

07-JAN-1997;

EP786519-A2 30-JUL-1997 05-JAN-1996;

Barash SC, Rosen CA;

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Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
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Scalato E, Scarselli M;
                                                                                                                                                                                                                                                                                                                                           AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
                                                                                                                                                                              606 TTAATCCAGTCAGGCAAATCTCTAAAACGTGTGATATTTGGACGAATTGCACCTCGGAAA
                                                                              663 ATGCCACCAGTACAGTACGTAACC---ACTTTTTATCTGCAAATAACGCTTTATTCTCT
                                                                                                                                                                                                                          27 AsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 Ala---ProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
                                                1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAla-
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Ratti G,
                                                                                                                                     17 LeuAlaSerCysAlaSerThr ------
    US-10-048-196-2 (1-134) x AAV74758 (1-1799)
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Tettelin H, Venter JC;
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98US-0094869.
98US-0098994.
98US-0099062.
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P-PSDB; AAY75498.
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02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                            Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fannon MR, Kunsch CA;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                   Staphylococcus aureus contig SEQ ID #447
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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AAV74758 standard; DNA; 1799 BP
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                                                                                       (first entry)
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represent
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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AA254537 to AA25456 and AA254616 to AA255473 repress PCR primers used in the exemplification of the present invention. The polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria for treating or preventing infection due to presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThr 36
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                                                                                                                                                                                                                                     Sequence 1731 BP; 507 A; 521 C; 418 G; 285 T; 0 other;
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Mismatches:
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01-NOV-2001

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Propionibacterium acres immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acres. The disorders include SAPHO syndrome (synovitis, acre, pustulosis, hypertosis and osteomyelitis), uveltis and endophthalmitis. P. acres is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acre vulgaris. A method for detecting the presence or absence of P acres in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patient comprises contacting a sample with a binding agent, that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypetides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypetides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAU55305-AAU55603 and AAU67567-AAU67570.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29139 BP; 6272 A; 9455 C; 8116 G; 5292 T; 4 other;
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                                                                                                                                                                                 DH, Mitcham JL,
ing Y, Jen S, Ca
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                                                        21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                 20-APR-2001; 2001WO-US12865.
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Propionibacterium acnes immunogenic polypeptides. The proteins and their
Expectated DNA sequences are used in the treatment, prevention and
clagnosis of medical conditions caused by P. acnes. The disorders include
Cd diagnosis of medical conditions caused by P. acnes. The disorders include
CC SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and
CC SAPHO syndrome, joints and the central nervous system, however it
CS particularly involved in the inflammatory lesions associated with acne
CC unigaris. A method for detecting the presence or absence of P. acnes in
CC patient comprises contacting a sample with a binding agent that binds to
CC the proteins of the invention and determining the amount of bound protein
CC antibodies specific for P. acnes proteins. These antibodies can be
CC antibodies specific for P. acnes proteins. These antibodies can be
CC antibodies specific for P. acnes proteins. These antibodies and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). This sequence encodes the
CC polypeptides shown in AAUS5503-AAUS5603 and AAUG7567-AAUG7570.
CNOLE: The sequence data for this patent did not form part of the printed
Specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                                                                              1822 CACCGGGCA-----TIGGTCAGAGTCTCCCAAAGTGGTGAAGGTCTTAGAGGCAATGATG 1875
                                                                                GluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsn 125
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               89 ValSerLeuThrGluLeuThrThrAlaAlaIleAsnPro-----AsnAlaArgThr
                                             Propionibacterium acnes immunogenic protein encoding DNA #64.
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Jen S, Carter D;
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               19482 AACCGTTTAAGGAACCCAGCACAAAGGCCCCGCCCTCCATAGCCATCAGC------TTG
                                                                                                                                                                                                                                                                                                                            44 ValLysGlnThrCysGln-----ThrGlnLeuThrGlyHisGlnTyrTrpLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCys
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                                                                                                                                                                                                                                          12 MetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnProLys--
Sequence 29139 BP; 6272 A; 9455 C; 8116 G; 5292 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #15441.
                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                             Indels:
                                                                                                                                                                Gaps:
                                                                                                                                                                                                    US-10-048-196-2 (1-134) x AAS59569 (1-29139)
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                                                        1.24e+03
81.00
47.15%
25.20%
11.98%
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19368 AGAGAAACA 19360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73
P-PSDB; ABG15450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 ArgHisSer 115
                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The colynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasmostics, forensics, gene mapping, identification of mutations can broad to produce other types of data and products dependent on DNA and considers of the invention invention which in medical equal products of the invention of the invention which in the produce of the invention invention which in the produce of the invention invention which in the produce of the invention invention invention in the produce of the invention invention invention invention in the produce of the invention invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1951 GGAACCATGGCCAGCTCCTGGATCTCTGCTCGCGTCTCCAGAGACTGTGGCAGGTGCAAG 1892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2128 TTTAGGATGGCCGGCTGTGGGACCTTCCCATCCCACGTCGACAGGAACATCAGGAGGTTC 2069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2011 AGTGTGTCCTGCACAATACCCATGACAGGCCGATTGCTCTGGGGGGGTGACAATCATGCGA 1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2068 ATCACTCCCCCCTCCAGGAAGACGTCTCTTGGTGAATTTG---CGCACTGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LeuSerSerGluSerLysAlaLysIleSer-GluThrAlaCysGlyCysVa
                                mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA differentially expressed in granulocytic cells #1187.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; granulocytic cell; DNA chip; bacterial infectio
viral infection; parasitic infection; protozoal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6732 BP; 1512 A; 2090 C; 1685 G; 1445 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1891 TTCATCTCATCCCGTCAAAGTCTGCATTGTACGGAGTTGTCA 1849
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Indels:
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Matches:
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                                                                                                                                        Claim 1; SEQ ID No 15441; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheThrLeuAlaSerCysAlaSerThrProGlu--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-048-196-2 (1-134) x AAS79637 (1-6732)
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80.00
46.32%
25.26%
11.83%
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Query Match:
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                                                                                         biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
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The invention relates to detecting (MI) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (GS) identified by
DNA chip analysis as given in the specification, and comparing
the expression level to an expression level in an unactivated
CC the comparing (M2) GA by contacting of with an agent
CC Also included are modulating (M2) GA by contacting GC with an agent
CC Also included are modulating (M3) GA or an inflammation (especially
CC for an agent capable of modulating CA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
Subject to a pathogen or sterile inflammatory disease using the
CC chronic) in a tissue, an allergic response in a subject, exposure of a
Subject to a pathogen or sterile inflammatory disease, by detecting the
CC chronic) in a tissue, an allergic response in a subject, exposure of a
Subject to a pathogen or sterile inflammatory disease, by detecting the
CC choice of expression of the gene is indicative of inflammation:
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from GS in the tissue. M1 is useful for detecting GA; M2 is useful for
CC contacting an inflammation in a tissue, an allergic
CC detecting an inflammation in a tissue, an allergic
CC detecting an inflammation in a contact to a pathogen
CC detecting an inflammation in a contact to a pathogen
CC detecting an inflammation in a tissue, an allergic
CC resource in a subject to a contacting of a contacting an agent capable of modulating
CC resource in a subject to a contacting of a contacting an inflammation in a contacting an agent capable of modulating
CC resource in a contacting an agent capable of modulating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, ARDS, adult respiratory distress syndrom, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection fungal infection and M5 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes.
                    rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel digease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
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fungal infection; sterile inflammatory disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 1187; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2000; 2000US-237189P.
                                                                                                                                                                                                                                                                                                                                                          03-OCT-2001; 2001WO-US30821
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46.32%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-435328/46.
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                                                                                                                                                                                        Homo sapiens.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                      2068 ATCACTICACCCCCCTCCAGGAAGACGTCTCTTGGTGAATTTG---CGCACTGCTGT 2012
                                                                                                                                                                                                                                                                  2011 AGTGTGTCCTGCACAATACCCATGACAGGCCGATTGCTCTGGGGGGTGACATCATGCGA 1952
                                                                                                                                                                                                                                                                                                                       1951 GGAACCATGGCCAGCTCCTGGATCTCTGCTCGCGTCTCCAGAGACTGTGCCAGGTGCAAG 1892
                                                                                                                                                                                                                                     64
                                                                                                     25
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                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                  65 ------LeuSerSerGluSerLysAlaLysIleSer-GluThrAlaCysGlyCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                   45 LysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLys
                                                                                                                                                                  26 ---SerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                    1891 ITCAICICATCCCCCTCAAAGICTGCAIIGIACGGAGIIGICA 1849
 38
                                                                                                                                                                                                                                                                                                                                                                    81 lAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThr 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #4116
Mismatches:
Indels:
                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 4116; 103pp; English.
                                                                                                 15 PheThrLeuAlaSerCysAlaSerThrProGlu-
                                                                US-10-048-196-2 (1-134) x ABK84616 (1-6732)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS68312 standard; cDNA; 6798 BP
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23-AUG-2000; 2000US-0649167
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25.26%
11.83%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food supplement;
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                 Query Match:
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a food supplement. (II).and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1954 GGAACCATGGCCAGCTCCTGGATCTCTGCTCGCGTCTCCAGAGACTGTGGCAGGTGCAAG 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| :::||| ||| :: ||| 2131 TTTAGGATGCCGGCTGTGGGAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2071 ATCACTTCACCCCCCTCCAGGAAGACGTCTTTTGTAATTTG---CGCACTGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 LysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------LeuSerSerGluSerLysAlaLysIleSer-GluThrAlaCysGlyCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysH1sAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N. meningitidis partial DNA sequence gnm_830 SEQ ID NO:830
                                                                                                                                                                                                                          Sequence 6798 BP; 1549 A; 2095 C; 1690 G; 1462 T; 2 other;
                                                                                                                                                                                                                                                                             6798
224
20
36
115
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                               15 PheThrLeuAlaSerCysAlaSerThrProGlu----
                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences
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99US-0132068
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46.32%
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                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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30-APR-1999;
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us-10-048-196-2.rng

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ABK35351 standard; cDNA; 2456

RESULT 24 ABK35351 ABK35351;

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represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AA882663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AA881259 and AAA81304 to AAA81312 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis Mens polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of bological probes, from the bacterium will also facilitate production of bological probes,
  Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presented targets for the immune system a which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance.
                                                                                                                            Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                   j immunogenic
to AAA82414
Scarselli M,
                                                                                                                                                                                                                                                                                             The present invention describes methods of obtaining proteins from Neisseria genomic sequences. AAA81453 t
  Ratti G,
                                                                                                                                                                                                                                          Claim 7; Page 1723; 1760pp; English.
  Mora M,
  Galeotti C,
                                                                            WPI; 2000-318079/27.
                            Rappuoli R,
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Sequence 783 BP; 214 A; 203 C; 197 G; 167 T; 2 other;

other more variable regions.

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LeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLySIleValArg 113
                                                                                                                                                                                                                                                                                                     140 TCCACCCACAAATAAAAAACGGCCCAAAACCAGCATGACTGCAACACTCAAGGGGTTA 199
                                                                                                                                                                                                                                                                                                                                                                                                                         ATCACGGCGCCAGGTATAAAAGCAATGGCAAGATTAAGGACGAAGCGGTTGGCTTTCCGG 298
                                                                                                                                                                                                                                         80 TCAATCGGACGCAATGCATCACATCGGCAATTTTAGGCTCTGCTCGGCTTTGGCGTTTC 139
                                                                                                                                                                                                                                                                                                                                 24 ProGluSerAsnProLysAsnSerSerAlaAsnLeu---ThrThrSerLeuIleLysHis 42
                                                                                                                                                                                                               43 AlaValLysGlnThrCysGlnThrGln-----LeuThrGlyHisGlnTyrTrpLysIle 60
                                                                                                                                                                   200 AACAGATACTCTTTGATTTGCCGAACAACAGCCCC------
                                                                                                                                                                                                                                                                       61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly---
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Conservative:
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Indels:
              Length:
                                                                                           Gaps:
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              12.5
79.50
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Alignment Scores:
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Conservative: Mismatches:

Percent Similarity: Best Local Similarity:

Query Match:

Indels:

US-10-048-196-2 (1-134) x ABK35351 (1-2456)

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The invention relates to 592 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins. The polynucleotides can be used as probes for the porteins of the polynucleotides and state of the length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease). Inflammatory disorders (e.g. Alzheimer's disease, parkinson's disease), linflammatory disorders (e.g. Conduls disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of
                                                                                                                                           viral infection; bacterial infection; fungal infection; diabetes; asthma; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour; autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer; coagulation disorder; inflammatory disorder; crohn's disease; incision; tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 burns, incisions and ulcers. The proteins are also useful for regulating haematopoiesis and for treating myeloid or lymphoid cell deficiencies. Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Five hundred and ninety two polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Resnick RJ;
                                                                                                                             gene; ss; nutritional supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 780 A; 471 C; 578 G; 627 T; 0 other;
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339
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Matches:
                                                                                          protein #489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fechtel K,
                                                                                          Human cDNA encoding secreted
                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2001; 2001WO-US10224.
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                                                    (first entry)
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                                                                                                                                 protein;
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K, Graham JR;
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                                                                                                                                 secreted
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                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                    08-MAY-2002
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more,genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                 1936 GCATAGCATCCAAAGTTAAAAGGGTTGTGCAACTAGCTCGAGAGGAAATCAAGAATGGAA 1995
                                                                                                                                                                                                                                              1876 TGAAGAAGTCCATGTGGGGTCAGTTCTGGTCTGCTCACCAGAGGTTCTTCAAATACTTAT 1935
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                                                                                                                Ser-LeulleLy
                                                                                                                                                                                                                            sile-AlaAlaMetLysLeuSerSerGluSerLysAlaLysileSerGluThrAlaCysG
                                                                                                                                                                                                                                                                                                               -----ACATTAGAAGCTTTGGAAGAGGGCGGGG
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MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
                                                                                                                                                                    sHisAlaValLys ----- GlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster expressed polynucleotide SEQ ID NO 10190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 10190; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   2125 ATTTCCTGCTCCAGACAAAAAAACTTTATAGTT 2160
                                                                                                                                                                                                                                                                                                                                                                                                119 Cys---MetLeuGluThrValAsnAlaPheIleVal 129
                                                                                                              -----AsnProLysAsnSerSerAlaAsnLeuThrThr
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                                                      21 AlaSerThrProGluSer------
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11-JUL-2000; 2000US-0614150.
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P-PSDB; ABB61133.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                      4294 CAA------TGGAAAACAGGCAGCAGAGGGGGGAAAATCCGGAAAAA 4335
                                                                                                                                                                                                                                                                                                                70
                                                                                                                                                                                                                                                                                                                                                                                                                    83
insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                      4336 GGGCGAGGATGCAGGAGGTCGTCTGTGGGGTAATTACGGACAAGTGCCGCACCATTAGCT
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                                                                                                                                                                                                                                                                                              31 SerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThr
                                                                                                                                                                                                                                                                                                                                                          GlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                            Sequence 10867 BP; 3008 A; 2450 C; 2315 G; 3094 T; 0 other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4396 TCCGCAAACAGTTTGTCC 4413
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2000US-0649167
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79.50
45.45%
228.79%
111.76%
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                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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23-AUG-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Second or the produce data for this parent did not appear in the printed specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                                                                                                                                                                                                                                                                 Sequence 13329 BP; 4337 A; 3011 C; 2943 G; 3038 T; 0 other;
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Matches:
Conservative:
Mismatches:
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12178 AAACATTCCATTGAA 12192
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening
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                                        WO200194629-A2
Homo sapiens
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28-SEP-2000;
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Soppet DR,
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an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                                                                                                                    Sequence 14770 BP; 4829 A; 3240 C; 3211 G; 3490 T; 0 other;
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Matches:
Conservative:
Mismatches:.
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2000US-233133P.
2000US-233617P.
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Best Local Similarity:
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18-SEP-2000;
18-SEP-2000;
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 847 sequences (given in ABLG166 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, descophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, squamous cell carcinoma, neuroendocrine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinoma, papillary carcinoma and Wilm's tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carter KC,
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2000US-235720P.
2000US-235840P.
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2000US-236028P.
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2000US-236111P.
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2000US-236891P.
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                                                     22-SEP-2000;
25-SEP-2000;
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Soppet DR,
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Sequence 14770 BP; 4829 A; 3240 C; 3211 G; 3490 T; 0 othqr;

Alignment Scores:

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11890
 stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                        11950 AGGGAT------AACATAATT-----GCAGTTAGAAAAGCATGTGCCACACAAAAG 11994
                                                                                                                                                                    11995 CAAGGG---CAGCCAGAGAAAGGCAAAGGCCAAACAGCTTCCATCCAAGTTGCCAGTAAAG 12051
                                                                                                                                                                                                       12112 ACTACCACCACCACCAGCTGCACAGTTAAAGTTAGGAAAAGTCAGGTCAAGGAAGTATGT 12171
                                                                                                                                                                                                                        93 GluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleVal 112
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                                                                                                                                                   53 ThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLys 72
                                                                              14 AlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnPro---LysAsnSerSer 32
                                                                                                                 33 AlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeu 52
                                                                                                                                                                                      73 IleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThr
                                                                                                                                                                                                                                                                                                                                                                                     cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                    Kidney cancer related gene sequence SEQ ID NO:6875.
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                            Gaps:
                                                            US-10-048-196-2 (1-134) x ABL68257 (1-14770)
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2000US-233617P.
2000US-234009P.
2000US-234034P.
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719
79.50
43.818
26.678
11.768
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                Percent Similarity:
Best Local Similarity:
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26-SEP-2000;
26-SEP-2000;
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in AbEG1664 to AbE70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical curvature and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, obesophageal, ovarian, kidney, prostate or pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
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Best Local Similarity:
27-SEP-2000;
28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
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28-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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P-PSDB; ABG21944
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                                                                                                                                                                                                                12112 ACTACCACCACCACCAGCTGCACAGTTAAAGTTAGGAAAAGTCAGCTCAAGGAAGTATGT 12171
                                        11950 AGGGAT-----AACATAATT-----GCAGTTAGAAAAGCATGTGCCACACAAAAG 11994
                                                                                                              93 GluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleVal 112
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33 AlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeu 52
                                                                                   53 ThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLys 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                        73 IleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #963.
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23-AUG-2000; 2000US-0649167
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P-PSDB; ABG00972.
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and to produce other types of data and products dependent on Di
amino acid sequences. AASG4197-AAS94564 represent novel human
diagnostic coding sequences of the invention.
Note: The sequence data for this patent did not appear in the
specification, but was obtained in electronic format directly
                                                                                                                                                                           Sequence 14797 BP; 3493 A; 3212 C; 3266 G; 4826 T; 0 other;
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Matches:
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Indels:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2.
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23-AUG-2000;
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                                                                                                                                                                                                                           Alignment Scores:
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponal and the constant of mattations of any analysis of sites expressing disorders involving aberrant protein expression of mattations chapter from the constant of mattations in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotides or other fraits to assess blodiversity are responsible for genetic disorders or other fraits to assess blodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11964 AGGGAT------AACATAATT-----GCAGTTAGAAAAGCATGTGCCACACAAAAG 12008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12066 GTAAGATCCACCTGTGTCACTACCACCACCACCACTGCCACCACCACCACCACTACCACC 12125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12126 ACTACCACCACCACCAGCTGCACGTTAAAGTTAGGAAAAGTCAGCTCAAGGAAGTATGT 12185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12009 CAAGGG---CAGCCAGAGAAAGGCAAGGCCAAACAGCTTCCATCCAAGTTGCCAGTAAAG 12065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 GluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLySIleVal 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 AlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 ThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 IleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThr
                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15187 BP; 4913 A; 3361 C; 3318 G; 3594 T; 1 other;
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52
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Mismatches:
Indels:
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                                                                                                                                               Claim 1; SEQ ID No 21935; 103pp; English
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43.81%
26.67%
11.76%
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Pred. No.:
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82144

Eropresent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81300 to AAA81303 and AAB2560 to AAA8565 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA8121 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis MenB polynuclectide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition on be used as a medicament (or in the manufacture of medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neisseriae. Identification of sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigent variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and
                                                                                                                                                                                                                                                                                                                                                                                                                               Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which are not antigenically variable or at least more conserved than
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            partial DNA sequence gnm_27 SEQ ID NO:27. ★
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Ratti G, Scarselli M,
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Indels:
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C, Mora M,
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79.50
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Rappuoli R, Pizza M;
                                                                                                                                         Veisseria meningitidis
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                 N. meningitidis
                                                                                                                                                                             WO200022430-A2.
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                                                                                                                                                                                                                                                              08-OCT-1999;
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30-APR-1999;
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The present invention describes the full length genome of Nelsseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 Nelsseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 from AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequences by 4980 bp (i.e. the last 49980 bp of AAF21644 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21648 encode the Nelsseria proteins given in AAB58550 to AAB58593, and AAF21588 encode the AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy.
                                                                                                     65624 TCCACCACAAAATAAAAAACGGCCCAAAACCAGCATGACTGCAACACTCAAGGGGTTA 65683
                                                                                                                                                                                                                                                    65723 ATCACGGCGGCGGCAGGTATAAAAGCAATGGCAAGATTAAGGACGAAGCGGTTGGCTTTCCGG 65782
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Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                  LeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArg 113
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frames are used to detect, treat and prevent Neisserial infections
 AlaValLysGlnThrCysGlnThrGln-----LeuThrGlyHisGlnTyrTrpLysIle
                                 65564 TCAATCGGACGCAATGCATCAACATCGGCAATTTTAGGCTCTGCTTGGCGTTTC
                                                                                                                                              -----CysValAlaAspLysAlaProGluAlaValSerLeuThrGlu
                                                                     61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly---
                                                                                                                                                                   Neisseria meningitidis B nucleotide sequence SEQ ID NO:108
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Scarlato V,
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                                                                                                                                                                                                                                                                                                                           65783 TCTTTTCCCAAGCCGTGC 65800
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08-OCT-1999; 99WO-US23573.
28-FEB-2000; 2000GB-0004695.
                                                                                                                                                                                                                                                                                         114 HisSerLeuLysProCys 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis.
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Galeotti C, Mora M,
Frazer CM, Grandi G;
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 43
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Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 115623 TCAATCGCAATGCATCAACATCGCAATTTAGGCTCTGCTCGCTTTGCCTTTC 115564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 115563 TCCACCCACAAAATAAAAAACCGCCCAAAAACCAGCATGATGACTGCAACACTCAAGGGGTTA 115504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 115464 ATCACGCGGCAGGTATAAAAGCAATGCCAAGATAAAGGACGAAGCGGTTGGCTTTCCGG 115405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 115683 CCCGAACGGGACGTACCCGGAACCAGTGCAAACACTTGGGCAACGCCGATCATCAAGGCA 115624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; ensyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly: --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 AlaValLysGlnThrCysGlnThrGln-----LeuThrGlyHisGlnTyrTrpLysIle
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                                                                                                                                                                                                                         Sequence 349980 BP; 84410 A; 84863 C; 94187 G; 86520 T; 0 other;
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                                                                                                                                                                                                                                                                                     349980
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17
46
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Mismatches:
Indels:
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Matches:
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2000US-208841P.
2000US-216747P.
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                                                                                                                                                                                                                                                                                   5.65e+04
79.50
40.57%
24.53%
11.76%
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Best Local Similarity:
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07-JUL-2000;
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AAS59666/
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AAS68171;
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AAS68171/c
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                                                                                                                                                                                                                                      Sequences AAS59506-AAS59804 represent DNA molecules encoding
Tropionibacterium acnes immunogenic polypeptides. The proteins and their
associated DNA sequences are used in the treatment, prevention and
diagnosis of medical conditions caused by D. acnes. The disorders include
SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and
osteomyelitis), uveitis and endophthalmitis. P acnes is also involved
in infections of bone, joints and the central nervous system, however it
sparticularly involved in the inflammatory lesions associated with acne
vulgaris. A method for detecting the presence or absence of P, acnes in a
patient comprises contacting a sample with a binding agent that binds to
the proteins of the invention and determining the amount of bound protein
in the sample. The polypeptides may be used as antigens in the production
of anthodies specific for P, acnes proteins. These antibodies can be
used to downregulate expression and activity of P, acnes, polypeptides and
therefore treat P, acnes infections. The antibodies may also be used as
diagnostic agents for determining P, acnes presence encodes the
polypeptides shown in AAUG5346-AAUG5355 and AAUG7770.

Note: The sequence data for this patient did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        679 CCGACCGTGGCCATAGTGCTGCCAGCCAGCTGCGTGCCGAAGACATCGACGTCGACGTC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGln 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       519 TCTTTGGACAACTGGGAGTGCGATGGCTACACACGGAGGCATCTACGCCGCCCTTGTCAC 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 LysIleValArgHisSerLeuLysPro------CysMetLeuGluThrValAsn 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
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                                                                                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnPro 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 LysAsnSerSerAlaAsnLeu-------ThrThrSerLeuIleLysHisAla 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      787 ACGACCAGTTCATCACCTGGGTGCCCTCTGACGGAGTCGGCCGCACAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CysValAlaAspLysAlaProGluAlaVal
                                       Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2243 BP; 435 A; 627 C; 753 G; 428 T; 0 other;
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39
18
61
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Mismatches:
Indels:
                                       Wang SS,
                                     Mitcham JL, Wang S:
Jen S, Carter D;
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Matches:
                                                                                                                                                                                                           Claim 1; SEQ ID No 161; 1069pp; English.
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                                 Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
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79.00
38.51%
26.35%
11.69%
                                                                                                                                                                     treating acne vulgaris -
(CORI-) CORIXA CORP.
                                                                                          WPI; 2001-616774/71
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The collection of collections are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful in medical inaging of sites expressing troot (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponance other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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36
19
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                                                                                                          126 AlaPhelleValProThrThr 133
                                                                                                                                                           508 GCACCGTTATCTCCTACGACCTCA 485
                                                                                                                                                                                                                                                                                                                                               AAS68171 standard; cDNA; 3300 BP
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23-AUG-2000; 2000US-0649167
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79.00
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P-PSDB; ABG03984.
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2471 CTGACATTCTGGGCCCATGCTCCAAGCCTTCTCTGGTTGTTGTCAGACTGCTCGGGAGCC 2412
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                                                                                                                                                                                                                                                                                                          91
                                                                       ---ThrLeuAlaSerCysAlaSer 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                  ---TrpLys
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                                                                                                                   23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle----
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                                                                                                                                                                                                                                                                                                                                                      ----ThrGluLeuThrThrAlaAlaIleAsnPro 101
  38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein; #6053.
  Mismatches:
Indels:
                                                                                                                                                                  -----LysHisAla------
                                                                    5 LeuTyrValThrAlaThrLeuMetThrAlaPhe---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 6053; 103pp; English.
                         Gaps:
                                             US-10-048-196-2 (1-134) x AAS68171 (1-3300)
                                                                                                                                                                                                                                                             ---IleAlaAlaMetLysLeuSer----
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ID AAS70249 standard; cDNA; 3300
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23-AUG-2000; 2000US-0649167
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P-PSDB; ABG06062.
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Best Local Similarity:
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            Query Match:
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polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The conjuctorides are also used in dagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques correstore normal activity of (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, teteracting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in companies, forensits, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and configuration sequences. AASS4197-AASS4564 represent novel human diagnostic coding sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO
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2411 AAACAATCCAAAGCCACTITGTGCACTGGCCATGAGGAATCACTGCTCAAGGACTGGAAA 2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2291 AGGTTGTCTGAGACAGCTCTCTTGCTTTCTCTCATACATTCTTAGCATAGTCCTCATG 2232
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Matches:
Conservative:
Mismatches:
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as foot for identifying appropriate in tissue, as molecular weight markers and as foot supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and on to produce other types of the invention.

Canno col sequences of the invention of mutations canno acid sequences of the invention.

Check the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
----SerGluSerLysAla 71
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23-AUG-2000; 2000US-0649167.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SerGluSerLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LeuTyrValThrAlaThrLeuMetThrAlaPhe-----ThrLeuAlaSerCysAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2471 CTGACATTCTGGGCCCATGCTCCAAGCCTTCTCTGGTTGTTGTCAGACTGCTCGGGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 LyslleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2231 GTAATAGTGCCTTGCTCTGAAAGAAAGACTTCAACCCCCAATCCA 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3300 BP; 1184 A; 745 C; 669 G; 702 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .---ThrGluLeuThrThrAlaAlaIleAsnPro 101
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                   Claim 1; SEQ ID No 10795; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-048-196-2 (1-134) x AAS74991 (1-3300)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS81666 standard; cDNA; 3300 BP
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79.00
40.74%
26.67%
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                                                                                                        biodiversity
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2471 CTGACATTCTGGGCCCATGCTCCAAGCCTTCTGTGTTGTTGTCAGACTGCTCGGGAGCC 2412
                                                                                                                                                                                                                                                                                                                 2411 AAACAATCCAAAGCCACTTGTGCACTGGCCATGAGCAATCACTGCTCAAGGACTGGAAA 2352
                                                                                                                                                                                                                                                                                                                                                                                       '60 ---IleAlaAlaMetLysLeuSer------SerGlu9erLysAla 71
                                                                                                                                                                                                                                                45 LysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyr----
                                                                                                         41 -------LysHisAla------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mappha, and in recombinant production of (II). The colymerises are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques correstore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a pulpeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in cappositic for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Committee the sequence data for this patent did not appear in the printed sequences the contains the printed sequence of the invention.
                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                      ONA encoding novel human diagnostic protein #17470.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 17470; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0540217
2000US-0649167.
                                                                 13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-639362/73
P-PSDB; ABG17479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2.
                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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23-AUG-2000;
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AAS81666;
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2291 AGGTTGTCTGAGACAGCTCTCTTGTTGTTTCTCTCATACATTCTTAGCATAGTCCTCATG 2232 72 LyslleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeu 2231 GTAATAGTGCCTTGCTCTGAAAGAAAGACTTCAACCCCCAATCCA 2187 92 ------ThrGluLeuThrThrAlaAlaIleAsnPro 101 Search completed: May 5, 2003, 23:24:15 Job time : 496 secs 2591 CTTTCCCTCACATCAACATTGATGGGCTCCATCAGAGTAACCTTTGCAGCAGTTGCATGC 2532 5 LeuTyrValThrAlaThrLeuMetThrAlaPhe-----ThrLeuAlaSerCysAlaSer 22 23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle----Conservative: Mismatches: Indels: Gaps: Length: Matches: US-10-048-196-2 (1-134) x AAS81666 (1-3300) 104 79.00 40.74% 26.67% 11.69% Best Local Similarity:

Percent Similarity:

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Query Match:

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